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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 31.4583 Seconds
(without alignments)
44.908 Million cell updates/sec

Title: US-09-753-139c-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|----------|--------------------|
| 1 | 34 | 100.0 | 5 | ABB83467 | Abb83467 Tissue In |
| 2 | 34 | 100.0 | 18 | AAR65010 | Aar65010 Tissue In |
| 3 | 34 | 100.0 | 20 | AAR31183 | Aar31183 N-termina |
| 4 | 34 | 100.0 | 36 | ABB38484 | Abb38484 Peptide # |
| 5 | 34 | 100.0 | 36 | AAM31928 | Aam31928 Peptide # |
| 6 | 34 | 100.0 | 36 | ABB23640 | Abb23640 Protein # |
| 7 | 34 | 100.0 | 36 | AAM71634 | Aam71634 Human bon |
| 8 | 34 | 100.0 | 36 | AAM59099 | Aam59099 Human bra |
| 9 | 34 | 100.0 | 36 | ABG53318 | Abg53318 Human liv |
| 10 | 34 | 100.0 | 36 | ABG41448 | Abg41448 Human pep |
| 11 | 34 | 100.0 | 42 | AAB25747 | Aab25747 Human sec |
| 12 | 34 | 100.0 | 47 | AAP60276 | Aap60276 N-termina |
| 13 | 34 | 100.0 | 48 | AAM48255 | Aam48255 Bovine me |
| 14 | 34 | 100.0 | 49 | ABB82136 | Abb82136 Bovine TI |
| 15 | 34 | 100.0 | 49 | ABB82135 | Abb82135 Human TIM |
| 16 | 34 | 100.0 | 57 | AAY70666 | Aay70666 Human tra |
| 17 | 34 | 100.0 | 83 | AAM87683 | Aam87683 Human imm |
| 18 | 34 | 100.0 | 102 | AAO02164 | Aao02164 Human pol |
| 19 | 34 | 100.0 | 115 | AAW85462 | Aaw85462 Secreted |
| 20 | 34 | 100.0 | 115 | ABP61805 | Abp61805 Human TIM |
| 21 | 34 | 100.0 | 127 | AAU99886 | Aau99886 Human TIM |
| 22 | 34 | 100.0 | 128 | AAU99887 | Aau99887 Human TIM |
| 23 | 34 | 100.0 | 151 | AAO07690 | Aao07690 A rat int |
| 24 | 34 | 100.0 | 151 | AAO07594 | Aao07594 A human i |
| 25 | 34 | 100.0 | 151 | ADB31994 | Adb31994 Human par |

| | | | | | | |
|----|----|-------|-----|---|-----------|--------------------|
| 26 | 34 | 100.0 | 160 | 3 | AAAY53891 | Aay53891 Partial a |
| 27 | 34 | 100.0 | 160 | 4 | AAG66120 | Agg66120 Human int |
| 28 | 34 | 100.0 | 162 | 5 | ABP42434 | Abp42434 Human ova |
| 29 | 34 | 100.0 | 173 | 3 | AAAY53893 | Aay53893 Partial a |
| 30 | 34 | 100.0 | 173 | 4 | AAG66122 | Agg66122 Human int |
| 31 | 34 | 100.0 | 174 | 6 | ABR58370 | AbR58370 Human NOV |
| 32 | 34 | 100.0 | 178 | 6 | ABR58369 | AbR58369 Human NOV |
| 33 | 34 | 100.0 | 183 | 3 | AAAB44149 | Aab44149 Human can |
| 34 | 34 | 100.0 | 183 | 3 | AAAY70658 | Aay70658 Mature mu |
| 35 | 34 | 100.0 | 183 | 6 | AAE36024 | Aae36024 Mouse int |
| 36 | 34 | 100.0 | 184 | 2 | AAE65000 | Aae65000 Chicken i |
| 37 | 34 | 100.0 | 184 | 5 | AAU99875 | Aau99875 Human tis |
| 38 | 34 | 100.0 | 185 | 3 | AAAY70656 | Aay70656 Mature hu |
| 39 | 34 | 100.0 | 185 | 6 | AAAB36020 | Aab36020 Human int |
| 40 | 34 | 100.0 | 186 | 3 | AAAY70655 | Aay70655 Mature hu |
| 41 | 34 | 100.0 | 186 | 6 | AAE36019 | Aae36019 Human int |
| 42 | 34 | 100.0 | 187 | 3 | AAAY70663 | Aay70663 Mature hu |
| 43 | 34 | 100.0 | 187 | 3 | AAAY70654 | Aay70654 Mature hu |
| 44 | 34 | 100.0 | 187 | 6 | AAAB36018 | Aab36018 Human int |
| 45 | 34 | 100.0 | 187 | 6 | AAAB36022 | Aab36022 Human int |

ALIGNMENTS

RESULT 1

ABB83467

ID ABB83467 standard; peptide; 5 AA.

XX ABB83467;

XX AC

XX DT

XX XX

30-SEP-2002 (first entry)

Tissue Inhibitor of Metalloproteinase, TIMP, derived peptide ChePep-6.

KWP; Matrix Metalloproteinase; zinc chelator; chronic wound; acute wound;

Tissue Inhibitor of Metalloproteinase; TIMP; connective tissue breakdown;

angiogenesis-associated disorder.

XX OS

Synthetic.

XX XX

WO200253173-A2.

XX PN

11-JUL-2002.

XX PD

21-DEC-2001; 2001WO-US049276.

XX PF

29-DEC-2000; 2000US-00753139.

XX PR

(KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PA

Quirk S, Tyrrell DJ;

XX PI

WPI; 2002-583595/62.

XX DR

New matrix metalloproteinase regulator useful for the treatment of chronic and acute wounds comprises a zinc chelator and a tissue inhibitor of metalloproteinases-derived peptide.

XX PT

Claim 6; Page 33; 57pp; English.

XX PS

The present invention relates to Matrix Metalloproteinase (MMP) regulators, which comprise a zinc chelator and a Tissue Inhibitor of Metalloproteinases (TIMP)-derived peptide. The present sequence is one such TIMP-derived peptide used to generate the MMP regulators. The MMP regulators are useful for treating chronic and acute wounds, angiogenesis-associated disorders; and other diseases and disorders involving uncontrolled breakdown of connective tissues by MMPs. MMPs contain a zinc molecule located in the active site, which participates in degrading collagen. The binding specificity of the TIMP-derived peptide brings the zinc chelator into molecular proximity of the MMP bound zinc in such a way to allow ligation. This results in the regulation of the level of MMP activity to promote wound healing by providing a MMP regulator having

CC high affinity and selectivity

XX Sequence 5 AA;

Query Match 100.0%; Score 34; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 |||||
 Db 1 CTCVP 5

RESULT 2

AAR65010
 ID AAR65010 standard; protein; 18 AA.

XX AC AAR65010;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 24-OCT-1995 (first entry)

XX DE Tissue inhibitor of metalloproteinase (TIMP-1) consensus.

XX KW Tissue inhibitor of metalloproteinase; diagnostic; therapeutic;
 prophylaxis.

XX KW Mammalia.

XX OS Key Location/Qualifiers

XX FT Inhibitory-site 2 /note= "Thr or Ser"

XX FT Misc-difference 4 /note= "Val or Ala"

XX FT Misc-difference 6 /note= "Pro or Thr"

XX FT Misc-difference 14 /note= "Asn or Ser"

XX FT Misc-difference 17 /note= "Ile or Val"

XX FT WO9505478-A1.

XX PD 23-FEB-1995.

XX PF 12-AUG-1994; 94WO-US009188.

XX PR 12-AUG-1993; 93US-00105263.

XX PR 13-DEC-1993; 93US-00167463.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Hawkes SP, Kishnani NS, Yang T;

XX DR WPI; 1995-098775/13.

XX PT New human tissue inhibitor of metalloproteinase-3 - used to develop

XX PT prods. for diagnosis, therapy or prophylaxis of conditions with unwanted

XX PT matrix metalloproteinase activity.

XX PS Disclosure; Fig 10; 87pp; English.

XX CC The sequence represents a consensus sequence for the N-terminal of tissue

XX CC inhibitor of metalloproteinase-1 (TIMP-1) from human, mouse, rabbit,

XX CC cattle, pig and rat. In the figure, the sequence is compared with the

XX CC human, chicken and mouse TIMP-3 N-terminals, and with consensus sequence

XX CC of TIMP-2 (AAR65011). A probe based on the ChIMP-3 amino acid sequence

XX CC (AAR65000) is used to isolate DNA encoding human TIMP-3 from a human cDNA

XX CC library. Human TIMP-3 can be used for the diagnosis, therapy or

XX CC prophylaxis of conditions characterized by excess or unwanted matrix

XX CC metalloproteinase activity, e.g. neoplasias, tumor metastasis,

XX CC inflammatory disorders such as rheumatoid arthritis, ulcerations,

CC reaction to infection, periodontal disease or osteoporosis. It can also
 CC be used in drug screening/design. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 34; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 |||||

Db 1 CTCVP 5

RESULT 3

AAR31183

ID AAR31183 standard; peptide; 20 AA.

XX AC AAR31183;

XX DT 25-MAR-2003 (revised)

XX DT 07-MAY-1993 (first entry)

XX DE N-terminal of monocyte specific chemotactic factor.

XX KW monocytes; leucocytes; white blood cells; neutrophils; chemotaxis;
 inhibition; tissue metalloproteinase inhibitor; tissue healing;

XX KW wound repair; infection; infectious disease; neoplasia; tumour; cancer;

XX KW gelatinase.

XX OS Synthetic.

XX FN WO9222664-A1.

XX PD 23-DEC-1992.

XX PF 10-JUN-1992; 92WO-EP001298.

XX PR 13-JUN-1991; 91IT-MI001634.

XX PA (DOMP-) DOMPE SPA.

XX PI Mantovani A, Bottazzi B, Bertini R, Van Damme J;

XX DR WPI; 1993-018147/02.

XX PT Chemotactic factor specific for monocytes - obtd. from human ovarian

XX PT cancer cell line, and used for treating infection and neoplasias and for

XX PT promoting tissue and wound repair.

XX PS Claim 1; Fig 2; 18pp; English.

XX CC This sequence represents the N-terminal of a chemotactic factor. The

XX CC factor is able to induce migration of monocytes, but not neutrophils, and

XX CC has an apparent molecular weight of 25kD on SDS-PAGE. The factor inhibits

XX CC tissue metalloproteinases, such as gelatinase, and concomitantly induces

XX CC chemotactic migration of monocytes. It can be used to promote tissue

XX CC repair or wound healing and for the treatment of infectious disorders and

XX CC neoplasias. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-

XX CC MAR-2003 to correct PR field.)

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 34; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 |||||

Db 1 CTCVP 5

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RESULT 4
ABB38484
ID ABB38484 standard; peptide; 36 AA.
XX
AC ABB38484;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #5990 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-48897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 32197; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 36 AA;
XX
Query Match 100.0%; Score 34; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 26 CTCVP 30
|||||

RESULT 6
ABB23640
ID ABB23640 standard; protein; 36 AA.
XX
AC ABB23640;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #5639 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

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RESULT 5
AAM31928
ID AAM31928 standard; protein; 36 AA.
XX
AC AAM31928;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5965 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX

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Query Match 100.0%; Score 34; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 26 CTCVP 30
|||||

RESULT 5
AAM31928
ID AAM31928 standard; protein; 36 AA.
XX
AC AAM31928;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #5965 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 26 CTCVP 30

RESULT 9
 ABG53318
 ID ABG53318 standard; peptide; 36 AA.
 XX AC ABG53318;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human liver peptide, SEQ ID No 31966.
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 XX KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US0000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
 XX PT gene expression in human adult liver.
 XX PS Claim 27; SEQ ID NO 31966; 658pp; English.
 XX CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 XX CC measuring human gene expression in a sample derived from human adult
 XX CC liver, comprising one of 13109 defined nucleotide sequences given in the
 XX CC specification (or complements/ fragments). The probe hybridises at high
 XX CC stringency to a nucleic acid molecule expressed in the human adult liver.
 XX CC (I) may be used for predicting, measuring and displaying gene expression
 XX CC in samples derived from human adult liver. The genes identified may be
 XX CC involved in genetic liver diseases such as cirrhosis,
 XX CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 XX CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 XX CC liver single exon encoded peptides of the invention. Note: The sequence
 XX CC information for this patent does not appear in the printed specification
 XX CC but was obtained in electronic format directly from WIPO at
 XX CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 34; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 26 CTCVP 30

RESULT 10
 ABG41448
 ID ABG41448 standard; peptide; 36 AA.
 XX AC ABG41448;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 31113.
 XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 XX KW chronic obstructive pulmonary disease; interstitial lung disease;
 XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 XX KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
 XX KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 XX KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 XX KW primary ciliary dyskinesia; pulmonary hypertension;
 XX KW hyaline membrane disease.
 XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US0000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX DR Spatially-addressable set of single exon nucleic acid probes, used to
 XX PT measure gene expression in human lung samples.
 XX PS Claim 27; SEQ ID NO 31113; 634pp; English.
 XX CC The invention relates to a spatially-addressable set of single exon
 XX CC nucleic acid probes for measuring gene expression in a sample derived
 XX CC from human lung comprising single exon nucleic acid probes having one of
 XX CC 12614 nucleic acid sequences mentioned in the specification, or their
 XX CC complements or the 12387 open reading frames derived from the 12614
 XX CC probes. Also included are a microarray comprising the novel set of probes
 XX CC; the novel set of probes which hybridise at high stringency to a nucleic
 XX CC acid expressed in the human lung; measuring gene expression in a sample
 XX CC derived from human lung, comprising (a) contacting the array with a
 XX CC collection of detectably labeled nucleic acids derived from human lung
 XX CC mRNA, and (b) measuring the label detectably bound to each probe of the
 XX CC array; identifying exons in a eukaryotic genome, comprising (a)
 XX CC algorithmically predicting at least one exon from genomic sequences of
 XX CC the eukaryote; and (b) detecting specific hybridisation of detectably
 XX CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 XX CC having a fragment identical to the predicted exon, the probe is included
 XX CC in the above mentioned microarray; assigning exons to a single gene,
 XX CC comprising (a) identifying exons from genomic sequence by the method
 XX CC above and (b) measuring the expression of each of the exons in several
 XX CC tissues and/or cell types using hybridisation to a single exon
 XX CC microarrays having a probe with the exon, where a common pattern of
 XX CC expression of the exons in the tissues and/or cell types indicates that
 XX CC the exons should be assigned to a single gene; a peptide comprising one
 XX CC of 12011 sequences, mentioned in the specification, or encoded by the
 XX CC probes/open reading frames (ORF). The probes are used for gene expression
 XX CC analysis, and for identifying exons in a gene, particularly using human

lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagenen syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 36 AA;

Query Match 100.0%; Score 34; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
|||||
Db 26 CTCVP 30

RESULT 11
AAB25747
ID AAB25747 standard; protein; 42 AA.

AC AAB25747;
XX
DT 04-DEC-2000 (first entry)

DE Human secreted protein sequence encoded by gene 23 SEQ ID NO:136.

Human: secreted protein; immunosuppressive; immunostimulant; nootropic; antiinflammatory; cardiac; vulnary; antitumor; anticonvulsant; antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovascular disorder; neurological disease; wound healing.

XX Homo sapiens.

XX WO2000043495-A2.

XX 27-JUL-2000.

XX 18-JAN-2000; 2000WO-US000903.

XX 19-JAN-1999; 99US-0116330P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Ebner R, Young PE, Ni J, Moore PA;

PI Komatsoulis G, Birze CE;

XX WPI; 2000-499225/44.

XX New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition.

XX Disclosure; Page 61; 45lpp; English.

XX The polynucleotide sequences given in AAB25666 to AAB25708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; immunostimulant; antiinflammatory; cardiac; vulnary; antitumor; nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective; antibacterial; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxis-

modulators and angiogenesis- modulators. The human secreted proteins and polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer, diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection. AAB25657 to AAB25665 and AAB25664 represent sequences used in the exemplification of the present invention

Sequence 42 AA;

Query Match 100.0%; Score 34; DB 3; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
|||||
Db 30 CTCVP 34

RESULT 12
AAP60276

ID AAP60276 standard; protein; 47 AA.

XX AC AAP60276;

XX 25-MAR-2003 (revised)

DT 03-OCT-2002 (revised)

DT 08-AUG-1991 (first entry)

DE N-terminal sequence of fibroblast derived purified human natural inhibitor of collagenases (NIC).

XX Metallo-proteinase inhibitor; wound healing; emphysema;
XX Rheumatoid arthritis therapy; ulceration; tumour metastasis.

XX Homo sapiens.

XX Synthetic.

XX EP189784-A.

XX 06-AUG-1986.

XX 16-JAN-1986; 86EP-00100482.

XX 18-JAN-1985; 85US-00692808.

XX (SEAR) SEARLE & CO G D.

XX Galloway WA, Clissold PM, McCullagh KG;

XX WPI; 1986-205910/32.

XX New human natural inhibitor of collagenase - for treating e.g. rheumatoid arthritis or ulceration, and new DNA sequences coding for it.

XX Example; Fig 5; 5lpp; English.

XX The patentors claim the AA SQ of human NIC, DNA sequences coding for NIC, and its RNA analogues and plasmids contg. this DNA. NIC inhibits the activity of metallo-proteinases, esp. of collagenase, proteoglycanase, gelatinase or a leucocyte, macrophage or tumour cell metallo-proteinase. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 47 AA;

Query Match 100.0%; Score 34; DB 1; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Metalloproteinase inhibitor; cytostatic; antirheumatic; antiarthritic;
 KW antianemic; neutroprotective; osteopathic; dermatological; vulnerary;
 KW gene therapy; angiogenesis; transgenic; human; TIMP.
 XX

OS Homo sapiens.

XX US2002090654-A1.

XX 11-JUL-2002.

XX 21-FEB-1997; 97US-00803954.

XX 19-MAY-1989; 89US-00355027.

XX 29-MAR-1990; 90US-00501904.

XX 03-JUN-1991; 91US-00710728.

XX 06-JUL-1993; 93US-00087021.

XX 11-MAR-1994; 94US-00212660.

XX (LANG/) LANGLEY K E.

XX (DECL/) DECLERCK Y A.

XX (BOON/) BOONE T C.

XX Langley KE, Declerck YA, Boone TC;

XX WPI; 2002-681724/73.

XX Novel purified and isolated metalloproteinase inhibitor polypeptide

XX useful for inhibiting tumor cell dissemination, for treating rheumatoid

XX arthritis, Paget's disease, osteoporosis, anemia and immunological

XX disorders.

XX Example 2; Page 10; 65pp; English.

XX The invention relates to a metalloproteinase inhibitor (MI) polypeptide.

XX The MI polypeptide is useful for inhibiting tumour cell dissemination or

XX for treating rheumatoid arthritis in a mammal. It is useful for treating

XX connective tissue disorders characterized by matrix degradation, for

XX treating disorders where excessive matrix losses are caused by

XX metalloproteinase activity, for promoting wound healing following surgery

XX or other wound situations, for treating dystrophic epidermolysis bullosa,

XX anemia, immunological disorders such as autoimmune disease (e.g. multiple

XX arthritis), for preventing or retarding tumour development, emphysema,

XX Paget's disease of bone, osteoporosis, scleroderma, pressure atrophy of

XX bone or tissues as in bedsores, cholesteatoma, and abnormal wound

XX healing. The DNA sequences are useful for effecting the large scale

XX synthesis of the polypeptide and in developing transgenic mammalian

XX species which may serve as eukaryotic hosts for production of MI and MI

XX products, and for identifying human MI gene disorders at the DNA level.

XX The present sequence represents a human TIMP (tissue inhibitor of

XX metalloproteinases) protein fragment

XX Sequence 49 AA;

XX Query Match

XX Best Local Similarity 100.0%; Score 34; DB 5; Length 49;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 1 CTCVP 5

Search completed: April 8, 2004, 11:10:04

Job time : 33.5583 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:02:14 ; Search time 9.09722 Seconds
(without alignments)
28.375 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34
Sequence: 1 CTCVP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A COMB.pap.*
2: /cgn2_6/prodata/2/iaa/5B COMB.pap.*
3: /cgn2_6/prodata/2/iaa/6A COMB.pap.*
4: /cgn2_6/prodata/2/iaa/6B COMB.pap.*
5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pap.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 34 | 100.0 | 15 | 1 | US-08-179-481-32 |
| 2 | 34 | 100.0 | 106 | 4 | US-09-452-817-2 |
| 3 | 34 | 100.0 | 151 | 4 | US-09-480-297A-6 |
| 4 | 34 | 100.0 | 160 | 4 | US-09-231-788-12 |
| 5 | 34 | 100.0 | 184 | 4 | US-09-452-817-1 |
| 6 | 34 | 100.0 | 202 | 4 | US-09-480-297A-8 |
| 7 | 34 | 100.0 | 202 | 4 | US-09-747-259-8 |
| 8 | 34 | 100.0 | 202 | 4 | US-09-816-744-8 |
| 9 | 34 | 100.0 | 205 | 4 | US-09-724-864-37 |
| 10 | 34 | 100.0 | 205 | 4 | US-09-480-297A-12 |
| 11 | 34 | 100.0 | 206 | 4 | US-08-134-231C-24 |
| 12 | 34 | 100.0 | 206 | 4 | US-08-728-160-24 |
| 13 | 34 | 100.0 | 207 | 1 | US-08-588-163-5 |
| 14 | 34 | 100.0 | 207 | 2 | US-09-111-070-5 |
| 15 | 34 | 100.0 | 207 | 4 | US-08-849-764C-5 |
| 16 | 34 | 100.0 | 207 | 4 | US-09-862-087-5 |
| 17 | 34 | 100.0 | 207 | 4 | US-08-463-261B-11 |
| 18 | 34 | 100.0 | 207 | 4 | US-09-540-530-1 |
| 19 | 34 | 100.0 | 207 | 4 | US-08-134-231C-22 |
| 20 | 34 | 100.0 | 207 | 4 | US-08-134-231C-23 |
| 21 | 34 | 100.0 | 207 | 4 | US-08-728-160-22 |
| 22 | 34 | 100.0 | 207 | 4 | US-08-728-160-23 |
| 23 | 34 | 100.0 | 212 | 4 | US-08-134-231C-29 |
| 24 | 34 | 100.0 | 212 | 4 | US-08-728-160-29 |
| 25 | 34 | 100.0 | 1079 | 3 | US-09-136-652-2 |
| 26 | 34 | 100.0 | 2409 | 6 | 5180808-2 |
| 27 | 33 | 97.1 | 20 | 4 | US-08-464-496-1 |

Sequence 1, Appli
Patent No. 5196194
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 179, App
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl

28 33 97.1 20 5 PCT-US92-07218-1
29 33 97.1 40 6 5196194-8
30 33 97.1 92 3 US-09-193-104-3
31 33 97.1 92 3 US-09-193-104-4
32 33 97.1 92 3 US-09-193-104-5
33 33 97.1 92 3 US-09-193-104-6
34 33 97.1 140 4 US-09-247-155-179
35 33 97.1 154 3 US-09-193-104-7
36 33 97.1 154 3 US-09-193-104-8
37 33 97.1 154 3 US-09-193-104-9
38 33 97.1 154 3 US-09-193-104-10
39 33 97.1 154 3 US-09-193-104-11
40 33 97.1 154 3 US-09-193-104-12
41 33 97.1 154 3 US-09-193-104-13
42 33 97.1 154 3 US-09-193-104-14
43 33 97.1 154 3 US-09-193-104-15
44 33 97.1 154 3 US-09-193-104-16
45 33 97.1 154 3 US-09-193-104-17

ALIGNMENTS

RESULT 1
US-08-179-481-32
; Sequence 32, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CARROTHERS, CARRAWAY, CORALIE A.
; APPLICANT: FREGIEN, NEVIS L.
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,481
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,521
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-179-481-32

Query Match 100.0%; Score 34; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 9 CTCVP 13

RESULT 2

US-09-452-817-2
 ; Sequence 2, Application US/09452817
 ; Patent No. 6342374
 ; GENERAL INFORMATION:
 ; APPLICANT: Carmichael, David F
 ; APPLICANT: Anderson, David C
 ; APPLICANT: Stricklin, George P
 ; APPLICANT: Welgus, Howard G
 ; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
 ; TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
 ; FILE REFERENCE: Manufacture Of Same
 ; FILE REFERENCE: Serial No. 6342374 09/452,817
 ; CURRENT APPLICATION NUMBER: US/09/452,817
 ; CURRENT FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 08/474,553
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/050,739
 ; PRIOR FILING DATE: 1993-04-21
 ; PRIOR APPLICATION NUMBER: 07/853,018
 ; PRIOR FILING DATE: 1992-03-18
 ; PRIOR APPLICATION NUMBER: 07/517,475
 ; PRIOR FILING DATE: 1990-05-01
 ; PRIOR APPLICATION NUMBER: 07/320,923
 ; PRIOR FILING DATE: 1989-03-08
 ; PRIOR APPLICATION NUMBER: 06/784,319
 ; PRIOR FILING DATE: 1985-10-04
 ; PRIOR APPLICATION NUMBER: 06/699,181
 ; PRIOR FILING DATE: 1985-02-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-452-817-2

Query Match 100.0%; Score 34; DB 4; Length 106;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 1 CTCVP 5

RESULT 3

US-09-480-297A-6
 ; Sequence 6, Application US/09480297A
 ; Patent No. 6562578
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorzan, Daniel M.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
 ; FILE REFERENCE: DX0917K
 ; CURRENT APPLICATION NUMBER: US/09/480,297A
 ; CURRENT FILING DATE: 2000-01-10
 ; PRIOR APPLICATION NUMBER: 60/115,506
 ; PRIOR FILING DATE: 1999-01-11
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-480-297A-6

Query Match 100.0%; Score 34; DB 4; Length 151;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 137 CTCVP 141

RESULT 4

US-09-231-788-12
 ; Sequence 12, Application US/09231788A
 ; Patent No. 6486301
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard
 ; TITLE OF INVENTION: Interleukin-20
 ; FILE REFERENCE: PF399P1
 ; CURRENT APPLICATION NUMBER: US/09/231,788A
 ; CURRENT FILING DATE: 1999-01-15
 ; EARLIER APPLICATION NUMBER: 60/052,870
 ; EARLIER FILING DATE: 1997-07-16
 ; EARLIER APPLICATION NUMBER: 60/055,952
 ; EARLIER FILING DATE: 1997-08-18
 ; EARLIER APPLICATION NUMBER: 60/060,140
 ; EARLIER FILING DATE: 1997-09-26
 ; EARLIER APPLICATION NUMBER: 09/115,832
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-231-788-12

Query Match 100.0%; Score 34; DB 4; Length 160;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 Db 125 CTCVP 129

RESULT 5

US-09-452-817-1
 ; Sequence 1, Application US/09452817
 ; Patent No. 6342374
 ; GENERAL INFORMATION:
 ; APPLICANT: Carmichael, David F
 ; APPLICANT: Anderson, David C
 ; APPLICANT: Stricklin, George P
 ; APPLICANT: Welgus, Howard G
 ; TITLE OF INVENTION: Human Collagenase Inhibitor, Recombinant Vector System
 ; TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
 ; FILE REFERENCE: Manufacture Of Same
 ; FILE REFERENCE: Serial No. 6342374 09/452,817
 ; CURRENT APPLICATION NUMBER: US/09/452,817
 ; CURRENT FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: 08/474,553
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/050,739
 ; PRIOR FILING DATE: 1993-04-21
 ; PRIOR APPLICATION NUMBER: 07/853,018
 ; PRIOR FILING DATE: 1992-03-18
 ; PRIOR APPLICATION NUMBER: 07/517,475
 ; PRIOR FILING DATE: 1990-05-01
 ; PRIOR APPLICATION NUMBER: 07/320,923
 ; PRIOR FILING DATE: 1989-03-08
 ; PRIOR APPLICATION NUMBER: 06/784,319
 ; PRIOR FILING DATE: 1985-10-04
 ; PRIOR APPLICATION NUMBER: 06/699,181
 ; PRIOR FILING DATE: 1985-02-05

; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 184
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-452-817-1

Query Match 100.0%; Score 34; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
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 Db 1 CTCVP 5

RESULT 6

US-09-480-297A-8
 ; Sequence 8, Application US/09480297A
 ; Patent No. 6562578
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Daniel M.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelein, Robert A.
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
 ; FILE REFERENCE: DK0917K
 ; CURRENT APPLICATION NUMBER: US/09/480,297A
 ; CURRENT FILING DATE: 2000-01-10
 ; PRIOR APPLICATION NUMBER: 60/115,506
 ; PRIOR FILING DATE: 1999-01-11
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 202
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-480-297A-8

Query Match 100.0%; Score 34; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 167 CTCVP 171

RESULT 7

US-09-747-259-8
 ; Sequence 8, Application US/09747259
 ; Patent No. 6569645
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: VanLookeren, Menno
 ; APPLICANT: Vandlen, Richard
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C1P1(US)
 ; CURRENT APPLICATION NUMBER: US/09/747,259

; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US 09/311,832
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US 60/172,096
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/31274
 ; PRIOR FILING DATE: 1999-12-30
 ; PRIOR APPLICATION NUMBER: US 60/175,481
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/04341
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: US 60/191,007
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/07532
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: US 60/213,087
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: US 09/644,848
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/242,837
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US00/30873
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: US 60/253,646
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO 8
 ; LENGTH: 202
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-747-259-8

Query Match 100.0%; Score 34; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 167 CTCVP 171

RESULT 8

US-09-816-744-8
 ; Sequence 8, Application US/09816744
 ; Patent No. 6579520
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: VanLookeren, Menno
 ; APPLICANT: Vandlen, Richard
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C1P2(US)
 ; CURRENT APPLICATION NUMBER: US/09/816,744

; CURRENT FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 8
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-8

Query Match 100.0%; Score 34; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 167 CTCVP 171

RESULT 9
US-09-724-864-37
; Sequence 37, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-37

Query Match 100.0%; Score 34; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 174 CTCVP 178

RESULT 10
US-09-480-297A-12
; Sequence 12, Application US/09480297A
; Patent No. 6562578
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-480-297A-12

Query Match 100.0%; Score 34; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVP 5
Db 174 CTCVP 178

RESULT 11
US-08-134-231C-24
; Sequence 24, Application US/08134231C
; Patent No. 6562596
; GENERAL INFORMATION:
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Koski, Raymond A.
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
; Three (TIMP-3) Composition and Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/134,231C
; APPLICATION NUMBER: US/08/134,231C
; FILING DATE: 06-Oct-1993
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-134-231C-24
Query Match 100.0%; Score 34; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTCVP 5
Db 24 CTCVP 28

RESULT 12
US-08-728-160-24
; Sequence 24, Application US/08728160
; Patent No. 6683155
; GENERAL INFORMATION:
; APPLICANT: Silbiger, Scott M.
; APPLICANT: Koski, Raymond A.
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
; Three (TIMP-3) Composition and Methods
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc./Patent Operations/KMP
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/728,160
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/134,231
;; FILING DATE:
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 206 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-728-160-24

Query Match 100.0%; Score 34; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 24 CTCVP 28

RESULT 13
US-08-588-163-5
; Sequence 5, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-1

US-08-588-163-5

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 24 CTCVP 28

RESULT 14
US-09-111-070-5
; Sequence 5, Application US/09111070
; Patent No. 5914392
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,070
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/588,163
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIMP-1
; US-09-111-070-5

Query Match 100.0%; Score 34; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 24 CTCVP 28

RESULT 15
US-08-849-764C-5
; Sequence 5, Application US/08849764C
; Patent No. 6300310

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; GENERAL INFORMATION:
; APPLICANT: GREENE, JOHN M
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; METALLOPROTEINASE-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,764C
; FILING DATE: 19-Sep-1997
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PFI48US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-849-764C-5

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Query Match          100.0%; Score 34; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. NO. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qv 1 CTCVP 5
Db 24 CTCVP 28

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Search completed: April 8, 2004, 11:20:31
Job time : 10.0972 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:16:30 ; Search time 21.6667 Seconds
(without alignments)
60.678 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 34 | 100.0 | 5 | 10 | US-09-753-139C-8 |
| 2 | 34 | 100.0 | 36 | 9 | US-09-864-761-38938 |
| 3 | 34 | 100.0 | 54 | 12 | US-10-424-599-213246 |
| 4 | 34 | 100.0 | 61 | 12 | US-10-424-599-279533 |
| 5 | 34 | 100.0 | 87 | 12 | US-10-424-599-236048 |
| 6 | 34 | 100.0 | 115 | 9 | US-09-745-763-46 |
| 7 | 34 | 100.0 | 127 | 14 | US-10-025-514-22 |
| 8 | 34 | 100.0 | 128 | 14 | US-10-025-514-24 |
| 9 | 34 | 100.0 | 151 | 14 | US-10-366-791-6 |
| 10 | 34 | 100.0 | 153 | 12 | US-10-428-114-40481 |
| 11 | 34 | 100.0 | 160 | 9 | US-09-731-816-4 |
| 12 | 34 | 100.0 | 160 | 10 | US-09-320-713-4 |
| 13 | 34 | 100.0 | 160 | 14 | US-10-153-770-4 |
| 14 | 34 | 100.0 | 160 | 14 | US-10-277-726A-12 |
| 15 | 34 | 100.0 | 160 | 14 | US-10-397-282-4 |

| | | | | | | |
|----|----|-------|-----|----|--------------------|-------------------|
| 16 | 34 | 100.0 | 162 | 15 | US-10-264-049-3566 | Sequence 3566, Ap |
| 17 | 34 | 100.0 | 173 | 9 | US-09-731-816-32 | Sequence 32, Appl |
| 18 | 34 | 100.0 | 173 | 10 | US-09-320-713-32 | Sequence 32, Appl |
| 19 | 34 | 100.0 | 173 | 14 | US-10-153-770-32 | Sequence 32, Appl |
| 20 | 34 | 100.0 | 173 | 14 | US-10-397-282-32 | Sequence 32, Appl |
| 21 | 34 | 100.0 | 174 | 12 | US-10-262-839-16 | Sequence 16, Appl |
| 22 | 34 | 100.0 | 178 | 12 | US-10-262-839-14 | Sequence 14, Appl |
| 23 | 34 | 100.0 | 183 | 9 | US-09-925-301-1594 | Sequence 1594, Ap |
| 24 | 34 | 100.0 | 184 | 14 | US-10-025-514-6 | Sequence 6, Appli |
| 25 | 34 | 100.0 | 199 | 12 | US-10-210-172-6 | Sequence 6, Appli |
| 26 | 34 | 100.0 | 199 | 12 | US-10-210-172-8 | Sequence 8, Appli |
| 27 | 34 | 100.0 | 202 | 9 | US-09-874-503-8 | Sequence 8, Appli |
| 28 | 34 | 100.0 | 202 | 10 | US-09-816-744-8 | Sequence 8, Appli |
| 29 | 34 | 100.0 | 202 | 10 | US-09-747-259-8 | Sequence 8, Appli |
| 30 | 34 | 100.0 | 202 | 10 | US-09-908-827-8 | Sequence 8, Appli |
| 31 | 34 | 100.0 | 202 | 12 | US-10-219-535-88 | Sequence 88, Appl |
| 32 | 34 | 100.0 | 202 | 12 | US-10-232-230-88 | Sequence 88, Appl |
| 33 | 34 | 100.0 | 202 | 12 | US-10-408-385-8 | Sequence 88, Appl |
| 34 | 34 | 100.0 | 202 | 13 | US-10-000-157-8 | Sequence 8, Appli |
| 35 | 34 | 100.0 | 202 | 14 | US-10-227-884-88 | Sequence 88, Appl |
| 36 | 34 | 100.0 | 202 | 14 | US-10-230-163-88 | Sequence 88, Appl |
| 37 | 34 | 100.0 | 202 | 14 | US-10-230-338-88 | Sequence 88, Appl |
| 38 | 34 | 100.0 | 202 | 14 | US-10-218-631-88 | Sequence 88, Appl |
| 39 | 34 | 100.0 | 202 | 14 | US-10-230-414-88 | Sequence 88, Appl |
| 40 | 34 | 100.0 | 202 | 14 | US-10-216-159A-88 | Sequence 88, Appl |
| 41 | 34 | 100.0 | 202 | 14 | US-10-218-849-88 | Sequence 88, Appl |
| 42 | 34 | 100.0 | 202 | 14 | US-10-227-873-88 | Sequence 88, Appl |
| 43 | 34 | 100.0 | 202 | 14 | US-10-227-883-88 | Sequence 88, Appl |
| 44 | 34 | 100.0 | 202 | 14 | US-10-219-076-88 | Sequence 88, Appl |
| 45 | 34 | 100.0 | 202 | 14 | US-10-230-434-88 | Sequence 88, Appl |

ALIGNMENTS

RESULT 1

US-09-753-139C-8
; Sequence 8, Application US/09753139C

; Publication No. US20030073808A1

; GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen

; APPLICANT: Tyrrell, David

; TITLE OF INVENTION: Design and Use of Advanced Zinc Chelating Peptides to Regulate Ma

; TITLE OF INVENTION: Metalloproteases

; FILE REFERENCE: 44039-227522 11301-0200

; CURRENT APPLICATION NUMBER: US/09/753,139C

; CURRENT FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

US-09-753-139C-8

Query Match 100.0%; Score 34; DB 10; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 1 CTCVP 5

RESULT 2

US-09-864-761-38938

; Sequence 38938, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

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; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: AeomIca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38938
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004087.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
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US-09-864-761-38938
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Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 26 CTCVP 30

RESULT 3
US-10-424-599-213246
; Sequence 213246, Application US/10424599
; Publication No. US20040031072A1
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: La Rosa Thomas J
; GENERAL INFORMATION:
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 213246
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_34586C.1.pep
; US-10-424-599-213246
Query Match 100.0%; Score 34; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 35 CTCVP 39

RESULT 4
US-10-424-599-279533
; Sequence 279533, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 279533
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_94440C.1.pep
; US-10-424-599-279533
Query Match 100.0%; Score 34; DB 12; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 15 CTCVP 19

RESULT 5
US-10-424-599-236048
; Sequence 236048, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
```

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 236048
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_5517C.1.pcp
US-10-424-599-236048

Query Match 100.0%; Score 34; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 28 CTCVP 32

RESULT 6

US-09-745-763-46
; Sequence 46, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; LaVallie, Edward R.
; Collins-Racie, Lisa A.
; Evans, Cheryl
; Merberg, David
; Treacy, Maurice
; Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 219
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/745,763

FILING DATE: 18-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sprunger, Suzanne A.

REGISTRATION NUMBER: 41,323

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 115 amino acids

TYPE: amino acid

STRANDEDNESS: <unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 46:

US-09-745-763-46

Query Match 100.0%; Score 34; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 48 CTCVP 52

RESULT 7

US-10-025-514-22
; Sequence 22, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:

APPLICANT: Philip J. BARR
; Applicant: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; FILE REFERENCE: 368292000200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-22

Query Match 100.0%; Score 34; DB 14; Length 127;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 2 CTCVP 6

RESULT 8

US-10-025-514-24
; Sequence 24, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:

APPLICANT: Philip J. BARR
; Applicant: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; FILE REFERENCE: 368292000200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-24

Query Match 100.0%; Score 34; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 2 CTCVP 6

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RESULT 9
US-10-366-791-6
; Sequence 6, Application US/10366791
; Publication No. US20030170827A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/10/366,791
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/480,297A
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-791-6

Query Match      100.0%; Score 34; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      137 CTCVP 141

RESULT 10
US-10-425-114-40481
; Sequence 40481, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40481
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-013-H8_FLI.pep
US-10-425-114-40481

Query Match      100.0%; Score 34; DB 12; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      143 CTCVP 147

RESULT 11
US-09-731-816-4
; Sequence 4, Application US/09731816
; Patent No. US20010023070A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/09/731,816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-4

Query Match      100.0%; Score 34; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      125 CTCVP 129

RESULT 12
US-09-320-713-4
; Sequence 4, Application US/09320713
; Publication No. US20030003545A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-320-713-4

Query Match      100.0%; Score 34; DB 10; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      125 CTCVP 129

RESULT 13
US-10-153-770-4
; Sequence 4, Application US/10153770

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; Publication No. US20030092133A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; APPLICANT: Steven M. Ruben
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/10/153,770
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-770-4

Query Match 100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 125 CTCVP 129

RESULT 14

US-10-277-726A-12
; Sequence 12, Application US/10277726A
; Publication No. US20030180892A1
; GENERAL INFORMATION:
; APPLICANT: Ebner et al.
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399P1D1
; CURRENT APPLICATION NUMBER: US/10/277,726A
; CURRENT FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: 09/231,788
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: 09/115,832
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/060,140
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-277-726A-12

Query Match 100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 125 CTCVP 129

RESULT 15

US-10-397-282-4
; Sequence 4, Application US/10397282

; Publication No. US20030186387A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/10/397,282
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US/09/731,816
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-397-282-4

Query Match 100.0%; Score 34; DB 14; Length 160;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 125 CTCVP 129

Search completed: April 8, 2004, 11:55:44
Job time : 21.6667 secs

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QM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 20.5556 Seconds

(without alignments)
76.748 Million cell updates/sec

Title: US-09-753-139C-8

Perfect score: 34

Sequence: 1 CTCVP 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 34 | 100.0 | 44 | 5 | Q7YVW4 |
| 2 | 34 | 100.0 | 44 | 5 | Q7YVU3 |
| 3 | 34 | 100.0 | 84 | 10 | Q9LRE1 |
| 4 | 34 | 100.0 | 106 | 5 | Q81632 |
| 5 | 34 | 100.0 | 121 | 12 | Q80NT4 |
| 6 | 34 | 100.0 | 169 | 4 | Q96QM2 |
| 7 | 34 | 100.0 | 196 | 11 | Q8K599 |
| 8 | 34 | 100.0 | 202 | 4 | Q8TAD2 |
| 9 | 34 | 100.0 | 205 | 11 | Q8K4C4 |
| 10 | 34 | 100.0 | 292 | 4 | Q96RY6 |
| 11 | 34 | 100.0 | 400 | 5 | Q9GRG2 |
| 12 | 34 | 100.0 | 487 | 5 | Q8MSX5 |
| 13 | 34 | 100.0 | 579 | 12 | Q98201 |
| 14 | 34 | 100.0 | 608 | 11 | Q8OV54 |
| 15 | 34 | 100.0 | 646 | 4 | Q8NEJ2 |
| 16 | 34 | 100.0 | 668 | 5 | Q9VAU4 |

| | | | | | | |
|----|----|-------|------|----|--------|--------------------|
| 17 | 34 | 100.0 | 670 | 4 | Q9Y6R3 | Q9Y6r3 homo sapien |
| 18 | 34 | 100.0 | 673 | 4 | Q86WK8 | Q86wk8 homo sapien |
| 19 | 34 | 100.0 | 721 | 5 | Q95YG0 | Q95yg0 ciona savig |
| 20 | 34 | 100.0 | 732 | 6 | Q95L62 | Q95l62 sus scrofa |
| 21 | 34 | 100.0 | 739 | 12 | Q9YQY1 | Q9yqy1 ranid herpe |
| 22 | 34 | 100.0 | 955 | 4 | Q96DN2 | Q96dn2 homo sapien |
| 23 | 34 | 100.0 | 995 | 4 | Q9NRZ1 | Q9nrz1 homo sapien |
| 24 | 34 | 100.0 | 1035 | 4 | Q15153 | Q15153 homo sapien |
| 25 | 34 | 100.0 | 1079 | 4 | Q9Y6R1 | Q9y6r1 homo sapien |
| 26 | 34 | 100.0 | 1079 | 4 | Q9UIC0 | Q9uic0 homo sapien |
| 27 | 34 | 100.0 | 1079 | 4 | Q9UIC1 | Q9uic1 homo sapien |
| 28 | 34 | 100.0 | 1079 | 4 | Q9H262 | Q9h262 homo sapien |
| 29 | 34 | 100.0 | 1079 | 4 | Q9UP50 | Q9up50 homo sapien |
| 30 | 34 | 100.0 | 1079 | 11 | Q9QYA6 | Q9qya6 rattus norv |
| 31 | 34 | 100.0 | 2146 | 5 | Q9VC97 | Q9vc97 drosophila |
| 32 | 34 | 100.0 | 7154 | 5 | Q81FD8 | Q81fd8 trypanosoma |
| 33 | 33 | 97.1 | 41 | 12 | Q9E2T0 | Q9e2t0 hepatitis b |
| 34 | 33 | 97.1 | 41 | 12 | Q9E2S4 | Q9e2s4 hepatitis b |
| 35 | 33 | 97.1 | 41 | 12 | Q9E2S8 | Q9e2s8 hepatitis b |
| 36 | 33 | 97.1 | 41 | 12 | Q9E2T1 | Q9e2t1 hepatitis b |
| 37 | 33 | 97.1 | 42 | 12 | Q80QT6 | Q80qt6 hepatitis b |
| 38 | 33 | 97.1 | 42 | 12 | Q80QT4 | Q80qt4 hepatitis b |
| 39 | 33 | 97.1 | 42 | 12 | Q80QT2 | Q80qt2 hepatitis b |
| 40 | 33 | 97.1 | 42 | 12 | Q80QT0 | Q80qt0 hepatitis b |
| 41 | 33 | 97.1 | 42 | 12 | Q80QS8 | Q80qs8 hepatitis b |
| 42 | 33 | 97.1 | 42 | 12 | Q80QS6 | Q80qs6 hepatitis b |
| 43 | 33 | 97.1 | 42 | 12 | Q80QS4 | Q80qs4 hepatitis b |
| 44 | 33 | 97.1 | 42 | 12 | Q80QS2 | Q80qs2 hepatitis b |
| 45 | 33 | 97.1 | 42 | 12 | Q80QS0 | Q80qs0 hepatitis b |

ALIGNMENTS

RESULT 1

| | | | |
|--|--------------|------|--------|
| Q7YVW4 | PRELIMINARY; | PRT; | 44 AA. |
| AC Q7YVW4; | | | |
| DT 01-OCT-2003 (TREMBlrel. 25, Created) | | | |
| DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update) | | | |
| DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update) | | | |
| DE Hypothetical protein. | | | |
| GN TB927.2.920. | | | |
| OS Trypanosoma brucei. | | | |
| OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma. | | | |
| OX NCBI_TaxID=5691; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RC STRAIN=Gutatio10.1; | | | |
| RA El-Sayed N.M.A., Ghedin E., Song J., Macleod A., Bringaud F., | | | |
| RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A., | | | |
| RA Biteau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E., | | | |
| RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G., | | | |
| RA Van Aken S., Utterback T., Haas B., Koo H.L., Umayam L., Suh B., | | | |
| RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblyum T., | | | |
| RA Salzberg S., Tait A., Turner M.R., Ullu E., White O., Melville S., | | | |
| RA Adams M.D., Fraser C.M., Donelson J.E.; | | | |
| RT "The sequence and analysis of Trypanosoma brucei chromosome II."; | | | |
| RL Nucleic Acids Res. 0:0-0(2003). | | | |
| DR EMBL; AF017167; AAQ15564.1; -- | | | |
| KW Hypothetical protein. | | | |
| SQ SEQUENCE 44 AA; 4912 MW; 8B51647E5A860A64 CRC64; | | | |

Query Match 100.0%; Score 34; DB 5; Length 44;

Best Local Similarity 100.0%; Pred. No. 6.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 14 CTCVP 18

RESULT 2

Q7YVU3
ID Q7YVU3 PRELIMINARY; PRT; 44 AA.
AC Q7YVU3; 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Hypothetical protein.
GN TB927.2.1280.
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUta10.1;
RA El-Sayed N.M.A., Ghedin E., Song J., MacLeod A., Bringaard F.,
RA Larkin C., Wanless D., Peterson J., Hou L., Taylor S., Tweedie A.,
RA Bateau N., Khalak H.G., Lin X., Mason T., Hannick L., Caler E.,
RA Blandin G., Bartholomeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,
RA Van Aken S., Uterback T., Haas B., Koo H.L., Umayam L., Suh B.,
RA Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblyum T.,
RA Salzberg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,
RA Adams M.D., Fraser C.M., Donelson J.E.;
RT "The sequence and analysis of Trypanosoma brucei chromosome II.";
RL Nucleic Acids Res. 0:0-0(2003).
DR EMBL; AE017167; AA015588.1; -.
KW Hypothetical protein.
SQ SEQUENCE 44 AA; 4840 MW; 8B51647CD0860A64 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 14 CTCVP 18

RESULT 3
Q9LRE1
ID Q9LRE1 PRELIMINARY; PRT; 84 AA.
AC Q9LRE1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE S locus protein 11-26 (Fragment).
GN SF11-26.
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S26(2-101);
RX MEDLINE=20273842; PubMed=10812061;
RA Watanabe M., Ito A., Takada Y., Nimomiya C., Kakizaki T., Takahata Y.,
RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satta Y., Shiba H.,
RA Takayama S., Isogai A.;
RT "Highly divergent sequences of the pollen self-incompatibility (S)
RT gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";
RL FEBS Lett. 473:139-144(2000).
DR EMBL; AB039755; BAA96393.1; -.
FT NON TER 1 1
SQ SEQUENCE 84 AA; 9469 MW; B34D639503CEC6A7 CRC64;

Query Match 100.0%; Score 34; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 65 CTCVP 69

RESULT 4
Q81632
ID Q81632 PRELIMINARY; PRT; 106 AA.
AC Q81632;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFL0065W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shailom S.J., Suh B., Peterson J., Angiuoli S.,
RA Partea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; AE014844; AAN36102.1; -.
KW Hypothetical protein.
SQ SEQUENCE 106 AA; 12267 MW; 6C6B54D391918E0A CRC64;

Query Match 100.0%; Score 34; DB 5; Length 106;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 22 CTCVP 26

RESULT 5
Q80NT4
ID Q80NT4 PRELIMINARY; PRT; 121 AA.
AC Q80NT4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE S protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retrod viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLD2235;
RA Gandhe S.S., Chadha M.S., Arankalle V.A.;
RT "Clinical manifestations and HBV genotypes and serotypes in western
RT India.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492222; AA084681.1; -.
DR GO; GO:0016032; P:Viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
FT NON TER 1 1
SQ SEQUENCE 121 AA; 13138 MW; C6E5C4FB7B944859 CRC64;

Query Match 100.0%; Score 34; DB 12; Length 121;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5

Db 104 CTCVP 108

|||||

RESULT 6

Q96QM2 PRELIMINARY; PRT; 169 AA.
 AC Q96QM2
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Tissue inhibitor of metalloproteinase 1 (Brythroid potentiating activity, collagenase inhibitor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007097; AAH07097.1; --
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 SQ SEQUENCE 169 AA; 18847 MW; 6C164206C87D815C CRC64;

Query Match 100.0%; Score 34; DB 4; Length 169;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 24 CTCVP 28

RESULT 7

Q8K599 PRELIMINARY; PRT; 196 AA.
 AC Q8K599
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Interleukin 27A precursor.
 GN IL17D OR IL27A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Hadj-Slimane R., Bobe P.;
 RT "Interleukin 27A (IL27A); a newly identified cytokine.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF502584; AAM33382.1; --
 DR MGD; MGI:2446510; IL17d.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 196 AA; 21124 MW; C350DFE028ABFC16 CRC64;

Query Match 100.0%; Score 34; DB 11; Length 196;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 165 CTCVP 169

RESULT 8

Q8TAD2 PRELIMINARY; PRT; 202 AA.
 AC Q8TAD2
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Interleukin 27 precursor (IL-17D) (Interleukin 17D).
 GN IL27.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Hadj-Slimane R., Bobe P.;
 RT "Interleukin 27 (IL27); a newly identified cytokine.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hromas R.A., Starnes T.T.;
 RT "IL-17D, A Novel Member of the IL-17 Family, Stimulates Cytokine Production and Inhibits Hematopoiesis.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY078238; AAL86911.1; --
 DR EMBL; AF479775; AAM12734.1; --
 DR EMBL; AF458062; AAM77566.1; --
 DR EMBL; BC036243; AAH36243.1; --
 DR Genew; HGNC:5984; IL17D.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 202 AA; 21893 MW; D171C5FB2DD039C3 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 167 CTCVP 171

RESULT 9

Q8K4C4 PRELIMINARY; PRT; 205 AA.
 AC Q8K4C4
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE IL-17D.
 GN IL17D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gilbert J.M., Gorman D.M.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF458063; AAM77567.1; --
 DR MGD; MGI:2446510; IL17d.

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SQ SEQUENCE 205 AA; 22390 MW; 6705746EF013318D CRC64;
Query Match 100.0%; Score 34; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 174 CTCVP 178

RESULT 10
Q96RY6 PRELIMINARY; PRT; 292 AA.
AC Q96RY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN GS114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL: AE006639; AAK61287.1; -.
KW Hypothetical protein.
SQ SEQUENCE 292 AA; 31183 MW; 785679B90314ABFA CRC64;

Query Match 100.0%; Score 34; DB 4; Length 292;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 160 CTCVP 164

RESULT 11
Q9GRG2 PRELIMINARY; PRT; 400 AA.
AC Q9GRG2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phenoloxidase activating factor.
GN PPAF.
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Larva;
RA MEDLINE=20467200; PubMed=11012672;
RA Kwon T.H., Kim M.S., Choi H.W., Joo C.H., Cho M.Y., Lee B.L.;
RT "A maquerade-like serine proteinase homologue is necessary for
RT phenoloxidase activity in the coleopteran insect, Holotrichia
RT glomphalia larvae.";
RL Eur. J. Biochem. 267:6188-6196(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AJ400904; CAC12696.1; -.
DR HSSP: P00763; IDPO.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
```

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DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR009003; Cys_Ser_trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 400 AA; 43754 MW; DEB882CB715D797 CRC64;

Query Match 100.0%; Score 34; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
Db 65 CTCVP 69

RESULT 12
Q8MSX5 PRELIMINARY; PRT; 487 AA.
AC Q8MSX5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE L013435P.
GN CRB OR CG6383.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarino H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY118509; AAM49878.1; -.
DR FlyBase; FBgn0000368; crb.
DR GO: GO:0016324; C:apical plasma membrane; NAS.
DR GO: GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO: GO:0007163; P:establishment and/or maintenance of cell po. .; IMP.
DR GO: GO:0016332; P:establishment and/or maintenance of polarit. .; IMP.
DR GO: GO:0016334; P:establishment and/or maintenance of polarit. .; IMP.
DR GO: GO:0045494; P:photoreceptor maintenance; IMP.
DR GO: GO:0042052; P:rhabdome development; NAS.
DR GO: GO:0045186; P:zonula adherens assembly; IMP.
DR GO: GO:0045218; P:zonula adherens maintenance; IMP.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR008985; ConA_like_lec_gl.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF-II.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001791; Laminin G.
DR Pfam; PF00008; EGF; 8.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 7.
```

DR PROSITE; PS01186; EGF_2; 6;
 DR PROSITE; PS01187; EGF_CA; 4;
 DR PROSITE; PS50025; LAM_G_DOMAIN; 1;
 KW EGF-like domain.
 SQ SEQUENCE 487 AA; 52498 MW; C69E5B14E36B3D22 CRC64;
 Query Match 100.0%; Score 34; DB 5; Length 487;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 241 CTCVP 245
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 RESULT 13
 ID Q98201 PRELIMINARY; PRT; 579 AA.
 AC Q98201;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MC0331.
 GN MC0331.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; PubMed=8670425;
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;
 RT "Genome sequence of a human tumorigenic poxvirus: Prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G., Moss B.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U60315; AAC55161.1; -;
 DR PIR; T30635; T30635.
 DR IncePro; IPR007110; Ig-like.
 SQ SEQUENCE 579 AA; 62626 MW; A37930DF92D311A3 CRC64;
 Query Match 100.0%; Score 34; DB 12; Length 579;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 63 CTCVP 67
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 RESULT 14
 ID Q80V54 PRELIMINARY; PRT; 608 AA.
 AC Q80V54;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE I300015B04Rik protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043473; AAH43473.1; -;
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx hydroxyl_S.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR006552; VC_out.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 3.
 DR Pfam; PF00093; vwc; 3.
 DR SMART; SM00181; EGF; 4.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00214; VWC; 3.
 DR SMART; SM00215; VWC_out; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS01208; VWF_1; 2.
 DR PROSITE; PS0184; VWF_2; 2.
 SQ SEQUENCE 608 AA; 64109 MW; 72E7136A82FF764F CRC64;
 Query Match 100.0%; Score 34; DB 11; Length 608;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 486 CTCVP 490
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 RESULT 15
 ID Q8NEJ2 PRELIMINARY; PRT; 646 AA.
 AC Q8NEJ2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Similar to solute carrier family 4, sodium bicarbonate cotransporter,
 DE member 4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030977; AAH30977.1; -;

DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005452; F:inorganic anion exchanger activity; IEA.
 DR GO; GO:0006820; P:anion transport; IEA.
 DR InterPro; IPR001717; Anion_exchange.
 DR InterPro; IPR003020; HCO3_cotransp.
 DR Pfam; PF00955; HCO3_cotransp; 1.
 DR PRINTS; PR01231; HCO3TRANSPORT.
 DR TIGREMS; TIGR00834; ae; 1.
 SQ SEQUENCE 646 AA; 72048 MW; 285D5E23C540A516 CRC64;

Query Match 100.0%; Score 34; DB 4; Length 646;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 |||||
 Db 583 CTCVP 587

Search completed: April 8, 2004, 11:16:20
 Job time : 21.5556 secs

F1-23/Domain: signal sequence #status predicted <SIG>
 F1-24-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
 F1-24-93,26-122,36-147,150-168,168-188/Disulfide bonds: #status predicted
 F1-53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
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 Db 24 CTCVP 28

RESULT 3
 ZYHUEP

metallopeptidase tissue inhibitor 1 precursor [validated] - human
 N/Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibitor
 C/Species: Homo sapiens (man)
 C/Date: 28-May-1986 #sequence revision 28-May-1986 #text change 08-Dec-2000
 C/Accession: A93372; A93363; A20595; A35826; A48417; S20318; S15872; I52912; S66
 R/Docherty, A.J.P.; Lyons, A.; Smith, B.J.; Wright, E.M.; Stephens, P.E.; Harris, T.J.R.
 Nature 318, 66-69, 1985
 A/Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to ex
 A/Reference number: A93372; MUID:86040463; PMID:3903517
 A/Accession: A93372
 A/Molecule type: mRNA
 A/Residues: 1-207 <DOC>
 A/Cross-references: GB:X03124; NID:G37182; PIDN:CAA26902.1; PID:G37183
 R/Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.
 Nature 315, 768-771, 1985
 A/Title: Molecular characterization and expression of the gene encoding human erythroid-
 A/Reference number: A93363; MUID:85240567; PMID:3839290
 A/Accession: A93363
 A/Molecule type: mRNA
 A/Residues: 1-207 <GAS>
 R/Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H.G.
 Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986
 A/Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
 A/Reference number: A23534; MUID:86205964; PMID:3010309
 A/Accession: A23534
 A/Molecule type: mRNA
 A/Residues: 1-207 <CAR>
 A/Cross-references: GB:M12670; NID:G182482; PIDN:AAA52436.1; PID:G182483
 A/Note: parts of this sequence were confirmed by protein sequencing
 A/Note: carbohydrate binding sites were determined
 R/Stricklin, G.P.; Welgus, H.G.
 J. Biol. Chem. 258, 12252-12256, 1983
 A/Title: Human skin fibroblast collagenase inhibitor.
 A/Reference number: A20595; MUID:84032401; PMID:6313647
 A/Accession: A20595
 A/Molecule type: protein
 A/Residues: 24-44, 'L', 46 <STR>
 A/Note: six disulfide bonds are present
 R/Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, K.
 DNA Cell Biol. 9, 479-485, 1990
 A/Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
 A/Reference number: A35826; MUID:91025550; PMID:2171551
 A/Accession: A35826
 A/Molecule type: mRNA
 A/Residues: 1-207 <RAP>
 R/Van Ranst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van
 Cytokine 3, 231-239, 1991
 A/Title: The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase an
 A/Reference number: A48417; MUID:91355647; PMID:1653055
 A/Accession: A48417
 A/Molecule type: protein
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-52 <VAN>
 A/Experimental source: monocytic cell line THP-1
 A/Note: sequence modified after extraction from NCBI backbone
 A/Note: sequence incorrectly identified as 96k gelatinase
 R/Osthues, A.; Knaeuper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.

FEBS Lett. 296, 16-20, 1992
 A/Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP)
 A/Reference number: S20318; MUID:92111776; PMID:1730286
 A/Accession: S20318
 A/Molecule type: protein
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-38 <OST>
 A/Experimental source: rheumatoid synovial fluid
 R/Opdenakker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.
 FEBS Lett. 284, 73-78, 1991
 A/Title: Natural human monocyte gelatinase and its inhibitor.
 A/Reference number: S15872; MUID:91285112; PMID:1647974
 A/Accession: S15872
 A/Molecule type: protein
 A/Residues: 'X', 25, 'X', 27-35, 'X', 37-42, 'X', 44, 'X', 46, 'X', 48-51 <FEB>
 A/Experimental source: peripheral blood monocytes
 R/Williamson, R.A.; Marston, F.A.O.; Angal, S.; Koklitis, P.; Panico, M.; Morris, H.R.;
 Biochem. J. 268, 267-274, 1990
 A/Title: Disulfide bond assignment in human tissue inhibitor of metalloproteinases (TIMP)
 A/Reference number: A38978; MUID:90303199; PMID:2163605
 A/Contents: annotation; disulfide bonds
 R/Opbroek, A.; Kenney, M.C.; Brown, D.
 Curr. Eye Res. 12, 877-883, 1993
 A/Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).
 A/Reference number: I52912; MUID:94123576; PMID:7507419
 A/Accession: I52912
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-207 <RES>
 A/Cross-references: GB:S68252; NID:G545022; PIDN:AAI4009.1; PID:G4261709
 R/Triebe, S.; Blaeser, J.; Gote, T.; Pelz, G.; Schueren, E.; Schmitt, M.; Tschesche, H.
 Eur. J. Biochem. 231, 714-719, 1995
 A/Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol
 A/Reference number: S66461; MUID:95377303; PMID:7649172
 A/Accession: S66461
 A/Molecule type: protein
 A/Residues: 24-38 <TRI>
 A/Experimental source: polymorphonuclear leukocytes
 C/Comment: This protein, found in a variety of body fluids, complexes with metalloprote
 s-specific, stimulating the growth and differentiation of only human and murine erythro
 C/Comment: The remarkable heat stability of this protein may be due to disulfide bond f
 C/Genetics:
 A/Gene: GDB:TIMP1; CLGI; TIMP
 A/Cross-references: GDB:119615; OMIM:305370
 A/Map position: Xp11.3-Xp11.23
 C/Superfamily: metalloproteinase inhibitor
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F1-24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
 F1-24-93,26-122,36-147,150-168,168-189/Disulfide bonds: #status experimental
 F1-53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 24 CTCVP 28

RESULT 4
 A35685
 metalloproteinase inhibitor 1 precursor - bovine
 N/Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhib
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 21-Sep-1990 #sequence revision 12-Apr-1996 #text_change 18-Jun-1999
 C/Accession: A35685; B34468; B29712; A34833; I46979
 R/Freudenstein, J.; Wagner, S.; Luck, R.M.; Einspanier, R.; Scheit, K.H.
 Biochem. Biophys. Res. Commun. 171, 250-256, 1990
 A/Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression
 A/Reference number: A35685; MUID:90365711; PMID:2393392
 A/Accession: A35685
 A/Molecule type: mRNA

A:Residues: 1-207 <PRE>
A:Cross-references: GB:M60073; NID:G163760; PIDN:AAA30784.1; PID:G163761
A:Experimental source: ovary cDNA library
R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.
J. Biol. Chem. 264, 17445-17453, 1989
A:Title: Purification and characterization of two related but distinct metalloproteinase
A:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:53.101/Binding site: carbohydrate (Asn) (covalent) #status predicted
A:Accession: B34468
A:Molecule type: protein
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>
A:Experimental source: culture medium of aortic endothelial cells
R:Kaczorek, M.; Honore, N.; Ribes, V.; Dehoux, P.; Cornet, P.; Cartwright, T.; Strecek,
Bio/Technology 5, 595-598, 1987
A:Title: Molecular cloning and synthesis of biologically active human tissue inhibitor o
A:Reference number: A34468; MUID:90008914; PMID:2551903
A:Accession: B34468
A:Molecule type: protein
A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>
A:Experimental source: culture medium of fibroblastic BC 21 cells
A:Note: protein inhibits angiogenesis
R:Moses, M.A.; Sudhalter, J.; Langer, R.
Science 248, 1408-1410, 1990
A:Title: Identification of an inhibitor of neovascularization from cartilage.
A:Reference number: A34833; MUID:90288433; PMID:1694043
A:Accession: A34833
A:Molecule type: protein
A:Residues: 24-51 <MOS>
A:Experimental source: cartilage
R:Sato, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.
Biol. Reprod. 50, 835-844, 1994
A:Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and ovidu
A:Reference number: I46979; MUID:94257757; PMID:8199264
A:Accession: I46979
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <SAT>
A:Cross-references: GB:S70841; NID:G546973; PIDN:AAB30892.1; PID:G546974
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F:24-93, 26-122, 36-147, 150-197, 155-160, 168-189/Disulfide bonds: #status predicted
F:53.101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
|||||
DB 24 CTCVP 28

RESULT 5
JC4303
matrix metalloproteinase-1 tissue inhibitor - baboon
C:Species: Papio sp. (baboon)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Jul-1999
C:Accession: JC4303
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lea, H.; Clowes, A.W.
Gene 163, 267-271, 1995
A:Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of
A:Reference number: JC4303; MUID:96011646; PMID:7590279
A:Accession: JC4303
A:Molecule type: mRNA
A:Residues: 1-207 <FOR>
A:Cross-references: GB:I37295; NID:G561545; PIDN:AAA99943.1; PID:G561546
A:Experimental source: smooth muscle cell

C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase fa
se and influences the proteinase activity. It has a role as a physiological molecule fo
C:Genetics:
A:Gene: timp-1
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F:53.101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 34; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
|||||
DB 24 CTCVP 28

RESULT 6
I46964
metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 19-Jan-2001
C:Accession: I46964
R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
Endocrinology 134, 344-352, 1994
A:Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases: c
eal tissue.
A:Reference number: I46964; MUID:94102210; PMID:8275949
A:Accession: I46964
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <SMI>
A:Cross-references: GB:S67450; NID:G456989; PIDN:AAB29472.1; PID:G456990
C:Superfamily: metalloproteinase inhibitor

Query Match 100.0%; Score 34; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
|||||
DB 24 CTCVP 28

RESULT 7
I47061
collagenase inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: I47061
R:Tanaka, T.; Andoh, N.; Takeya, T.; Sato, E.
Mol. Cell. Endocrinol. 83, 65-71, 1992
A:Title: Differential screening of ovarian cDNA libraries detected the expression of the
A:Reference number: I47061; MUID:92201478; PMID:1312961
A:Accession: I47061
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TAN>
A:Cross-references: GB:S96211; NID:G247729; PIDN:AAB21865.1; PID:G247730
C:Superfamily: metalloproteinase inhibitor

Query Match 100.0%; Score 34; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
|||||
DB 24 CTCVP 28

RESULT 8
A43429
metalloproteinase inhibitor 3 precursor - chicken

```

RESULT 10
T30635
hypothetical protein 33L - Molluscum contagiosum virus 1
N:Alternate names: MC033L
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text-
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus
A:Reference number: Z20876; MUID:96325459; PMID:8670425
A:Accession: T30635
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-579 <SEN>
A:Cross-references: EMBL:U60315; NID:g1491943; PIDN:AAC5
C:Genetics:
A:Note: MC033L
C:Superfamily: Molluscum contagiosum virus 1 hypothetical

```

```

Query Match      100.0%; Score 34; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTCVP 5
Db      63 CTCVP 67

```

```

RESULT 11
S43922
vserican - pig-tailed macaque (fragments)
N;Alternate names: chondroitin sulfate proteoglycan
C;Species: Macaca nemestrina (pig-tailed macaque)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Jul-1999
C;Accession: S43922

```

Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and
A;Reference number: S43921; MUID:95005762; PMID:7921538

A:Structure type: *unknA*
A:Residues: 1-233/234-525;526-862 <YAO>
A:Cross-references: EMBL:S72413
A:Note: 507-Ser was also found
A:Note: the authors translated the codon GCC for residue 50 as Val, AAG for residue 422
669 as Asn
C:Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG2
C:Keywords: chondroitin sulfate proteoglycan; extracellular matrix
F:1-37/Domain: link protein repeat homology (fragment) <LNK1>
F:58-139/Domain: link protein repeat homology <LNK2>
F:722-753/Domain: EGF homology <EG1>
F:760-791/Domain: EGF homology <EG2>

| | | | | |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match | 100.0% | Score 34; | DB 2; | Length 862; |
| Best Local Similarity | 100.0%; | Pred. No. 1.2e+02; | | |
| Matches 5; | Conservative | 0; | Mismatches 0; | Indels 0; |
| Matches 0; | Gaps | 0; | | |

| QY | 1 | CTCVP | 5 |
|----------------|-----|-------|-----|
| | | | |
| D _b | 742 | CTCVP | 746 |

RESULT 12

A40136
fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: epidermal growth factor homolog precursor
N;Contents: alternatively spliced fibropellin Ib (SGF1)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change
C;Accession: A40136; B40136; A29316; A43131
E;Delgadoillo-Reynoso, M.G.; Rollo, D.R.; Hersh, R.A.

C/Species: Strongylocentrotus purpuratus (purple urchin)
C/Date: 13-May-1992 #sequence revision 17-Sep-1997 #text_change 21-Jul-2000
C/Accession: A40136; B40136; C40136; D29316; A43131
R:Delgadillo-Reynoso, M.G.; Rollo, D.R.; Hursh, D.R.; Raff, R.A.
a/Comments: ultramarine spined abropopium 15 (b01),

J. Mol. Evol. 29, 314-327, 1989
 A:Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpurus
 A:Reference number: A40136; MUID:90112459; PMID:2514273
 A:Accession: A40136
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-114
 A:Cross-references: GB:M17530; NID:gl0225; PID:g667061
 A:Accession: B40136
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE>
 A:Accession: C40136
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 'K',747-821,898-978 <DE3>
 R:Hurch, D.A.; Andrews, M.E.; Raff, R.A.
 Science 237, 1487-1490, 1987
 A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
 A:Reference number: A29316; MUID:87319677; PMID:3498216
 A:Accession: A29316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 'S',280-481,786-1064 <HUR>
 A:Cross-references: GB:M17421; NID:gl61474; PIDN:AAA30050.1; PID:g552260
 R:Hunt, L.T.; Barker, W.C.
 PNAS 76, 1760-1764, 1979
 A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
 A:Reference number: A43131; MUID:89196806; PMID:2784773
 A:Contents: annotation
 C:Superfamily: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1064/Product: fibropellin I #status predicted <FIB>
 F:23-54/Domain: EGF homology <EG01>
 F:57-175/Domain: C1r/C1s repeat homology <C1R>
 F:180-211/Domain: C1r/C1s repeat homology <EG02>
 F:218-249/Domain: EGF homology <EG03>
 F:256-287/Domain: EGF homology <EG04>
 F:294-325/Domain: EGF homology <EG05>
 F:332-363/Domain: EGF homology <EG06>
 F:370-401/Domain: EGF homology <EG07>
 F:408-439/Domain: EGF homology <EG08>
 F:446-477/Domain: EGF homology <EG09>
 F:484-515/Domain: EGF homology <EG10>
 F:522-553/Domain: EGF homology <EG11>
 F:560-591/Domain: EGF homology <EG12>
 F:598-629/Domain: EGF homology <EG13>
 F:636-667/Domain: EGF homology <EG14>
 F:674-705/Domain: EGF homology <EG15>
 F:712-743/Domain: EGF homology <EG16>
 F:750-781/Domain: EGF homology <EG17>
 F:788-819/Domain: EGF homology <EG18>
 F:826-857/Domain: EGF homology <EG19>
 F:864-895/Domain: EGF homology <EG20>
 F:902-933/Domain: EGF homology <EG21>
 F:936-1064/Region: avidin-like
 F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
 57,451-466,468-477,484-495/Disulfide bonds: #status predicted
 F:489-504,506-515,522-533,527-542,544-553,560-571,598-609,603-618,620-62
 08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disul
 Query Match 100.0%; Score 34; DB 2; Length 1064;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 542 CTCVP 546
 RESULT 13
 PC7034

Na+ bicarbonate cotransporter - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
 C:Accession: PC7034
 R:Thevenod, F.; Roussa, E.; Schmitt, B.M.; Romero, M.F.
 Biochem. Biophys. Res. Commun. 264, 291-298, 1999
 A:Title: Cloning and immunolocalization of a rat pancreatic Na+ bicarbonate cotransporter
 A:Reference number: PC7034; MUID:99458660; PMID:10527880
 A:Accession: PC7034
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1079 <THE>
 A:Cross-references: GB:AF107265; NID:g6523792; PID:g6523793
 C:Genetics:
 A:Gene: nbc
 C:Superfamily: band 3 anion transport protein
 Query Match 100.0%; Score 34; DB 2; Length 1079;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 627 CTCVP 631
 RESULT 14
 T14274
 versican precursor, splice form V2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
 C:Accession: T14274
 R:Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
 J. Biol. Chem. 273, 15758-15764, 1998
 A:Title: Versican V2 is a major extracellular matrix component of the mature bovine brain
 A:Reference number: Z17954; MUID:98288320; PMID:9624174
 A:Accession: T14274
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1643 <SCH>
 A:Cross-references: EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC24360.1
 A:Experimental source: brain
 C:Keywords: glycoprotein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-1643/Product: versican, splice form V2 #status predicted <MAT>
 F:57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #st
 Query Match 100.0%; Score 34; DB 2; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 1360 CTCVP 1364
 RESULT 15
 A35672
 crumbs protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2003
 C:Accession: A35672
 R:Teppass, U.; Theres, C.; Knust, E.
 Cell 61, 787-799, 1990
 A:Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila
 A:Reference number: A35672; MUID:90263104; PMID:2344615
 A:Accession: A35672
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2139 <TEP>
 A:Cross-references: GB:M33753
 A:Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residu
 C:Genetics:

A:Gene: FlyBase:Crb
A:Cross-references: FlyBase:FBgn000368
C:Keywords: transmembrane protein
F:352-385/Domain: EGF homology <EGX1>
F:392-424/Domain: EGF homology <EGF1>
F:691-722/Domain: EGF homology <EGF>
F:767-799/Domain: EGF homology <EGF3>
F:1878-1914/Domain: EGF homology <EGX2>

Query Match 100.0%; Score 34; DB 2; Length 2139;
Best Local Similarity 100.0%; Pred. NO. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 1903 CTCVP 1907

Search completed: April 8, 2004, 11:18:08
Job time : 7.80556 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 11:00:44 ; Search time 4.16667 Seconds
(without alignments)
62.484 Million cell updates/sec

Title: US-09-753-139c-8
Perfect score: 34
Sequence: 1 CTCVP 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 34 | 100.0 | 206 | 1 TIM1_RABIT | P20614 oryctolagus |
| 2 | 34 | 100.0 | 207 | 1 TIM1_BOVIN | P20414 bos taurus |
| 3 | 34 | 100.0 | 207 | 1 TIM1_HORSE | O02722 equus caball |
| 4 | 34 | 100.0 | 207 | 1 TIM1_HUMAN | P01033 homo sapien |
| 5 | 34 | 100.0 | 207 | 1 TIM1_PAPCY | P49061 papio cynoc |
| 6 | 34 | 100.0 | 207 | 1 TIM1_PIG | P35624 sus scrofa |
| 7 | 34 | 100.0 | 207 | 1 TIM1_SHEEP | P50122 ovis aries |
| 8 | 34 | 100.0 | 212 | 1 TIM3_CHICK | P26552 gallus gall |
| 9 | 34 | 100.0 | 862 | 1 PGCY_MACNE | Q28858 macaca neme |
| 10 | 34 | 100.0 | 1064 | 1 FBPI_STRPU | P10079 strongyloce |
| 11 | 34 | 100.0 | 2139 | 1 CRB_DROME | P10040 drosophila |
| 12 | 34 | 100.0 | 3381 | 1 PGCY_BOVIN | P81282 bos taurus |
| 13 | 34 | 100.0 | 3396 | 1 PGCY_HUMAN | P13611 homo sapien |
| 14 | 33 | 97.1 | 226 | 1 VMSA_HBEVO | P13873 hepatitis b |
| 15 | 33 | 97.1 | 226 | 1 VMSA_HBEVD | P31868 hepatitis b |
| 16 | 33 | 97.1 | 226 | 1 VMSA_HBEVN | P30019 hepatitis b |
| 17 | 33 | 97.1 | 226 | 1 VMSA_HBEVS | P31869 hepatitis b |
| 18 | 33 | 97.1 | 389 | 1 VMSA_HBEVA | P24025 hepatitis b |
| 19 | 33 | 97.1 | 389 | 1 VMSA_HBEVI | P17397 hepatitis b |
| 20 | 33 | 97.1 | 389 | 1 VMSA_HBEVJ | P17398 hepatitis b |
| 21 | 33 | 97.1 | 389 | 1 VMSA_HBEVL | P12911 hepatitis b |
| 22 | 33 | 97.1 | 389 | 1 VMSA_HBEVO | P17399 hepatitis b |
| 23 | 33 | 97.1 | 389 | 1 VMSA_HBEVW | P03142 hepatitis b |
| 24 | 33 | 97.1 | 389 | 1 VMSA_HBEVY | P03138 hepatitis b |
| 25 | 33 | 97.1 | 389 | 1 VMSA_HBEVZ | P03139 hepatitis b |
| 26 | 33 | 97.1 | 400 | 1 VMSA_HBEV2 | P03141 hepatitis b |
| 27 | 33 | 97.1 | 400 | 1 VMSA_HBEV4 | P12934 hepatitis b |
| 28 | 33 | 97.1 | 400 | 1 VMSA_HBEV9 | P17101 hepatitis b |
| 29 | 33 | 97.1 | 400 | 1 VMSA_HBEVP | Q02317 hepatitis b |
| 30 | 33 | 97.1 | 400 | 1 VMSA_HBEVR | P03140 hepatitis b |
| 31 | 33 | 97.1 | 400 | 1 VMSA_HBEVT | O05496 hepatitis b |
| 32 | 31 | 91.2 | 214 | 1 TIM3_SCYTO | Q9w684 scyllorhinu |
| 33 | 31 | 91.2 | 376 | 1 FA10_HOBST | P83370 hoptiocephal |

| | | | | | |
|----|----|------|------|--------------|--------------------|
| 34 | 31 | 91.2 | 376 | 1 FA10_TROCA | P81428 tropidochis |
| 35 | 31 | 91.2 | 570 | 1 FBPI_STRPU | P49013 strongyloce |
| 36 | 31 | 91.2 | 666 | 1 MOD_DROME | P18105 drosophila |
| 37 | 31 | 91.2 | 686 | 1 DLL4_MOUSE | Q9j171 mus musculu |
| 38 | 31 | 91.2 | 1964 | 1 NTC4_MOUSE | P31695 mus musculu |
| 39 | 31 | 91.2 | 2003 | 1 NTC4_HUMAN | Q99466 homo sapien |
| 40 | 31 | 91.2 | 2524 | 1 NOTC_XENLA | P21783 xenopus lae |
| 41 | 31 | 91.2 | 3562 | 1 PGCY_CHICK | Q90953 gallus gall |
| 42 | 30 | 88.2 | 57 | 1 YC57_HAEIN | P41443 haemophilus |
| 43 | 30 | 88.2 | 92 | 1 LCM_LOCOMI | P80060 locusta mig |
| 44 | 30 | 88.2 | 158 | 1 VGO5_HSV11 | Q00163 ictalurid h |
| 45 | 30 | 88.2 | 162 | 1 BAR2_CHIPA | P08725 chironomus |

ALIGNMENTS

RESULT 1

| TIMI_RABIT | STANDARD; | PRT; | 206 AA. |
|--|-----------|------|--------------------------------|
| AC P20614; | | | |
| DT 01-FEB-1991 (Rel. 17, Created) | | | |
| DT 01-FEB-1991 (Rel. 17, Last sequence update) | | | |
| DT 15-MAR-2004 (Rel. 43, Last annotation update) | | | |
| DE Metalloproteinase inhibitor 1 precursor (TIMP-1). | | | |
| GN TIMP1. | | | |
| OS Oryctolagus cuniculus (Rabbit). | | | |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. | | | |
| OX NCBI_TaxID=9986; | | | |
| RN [1] | | | |
| RP SEQUENCE FROM N.A. | | | |
| RX MEDLINE=89214135; PubMed=2708356; | | | |
| RA Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Notter R.H., | | | |
| RA Horvitz D.J.; | | | |
| RT "Hyperoxic exposure alters gene expression in the lung. Induction of | | | |
| the tissue inhibitor of metalloproteinases mRNA and other mRNAs."; | | | |
| RL J. Biol. Chem. 264:7092-7095(1989). | | | |
| CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases) | | | |
| and irreversibly inactivates them. | | | |
| CC -!- SUBCELLULAR LOCATION: Secreted. | | | |
| CC -!- PTM: The activity of TIMP1 is dependent on the presence of | | | |
| disulfide bonds. | | | |
| CC -!- SIMILARITY: Belongs to the TIMP family. | | | |
| CC -!- SIMILARITY: Contains 1 NTR domain. | | | |
| CC This SWISS-PROT entry is copyright. It is produced through a collaboration | | | |
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| or send an email to license@isb-sib.ch). | | | |
| CC ----- | | | |
| EMBL; J04712; AAA31478.1; - | | | |
| DR PIR; A33350; A33350. | | | |
| DR HSSP; P01033; 1D2B. | | | |
| DR InterPro; IPR001820; TIMP. | | | |
| DR InterPro; IPR008993; TIMP_like. | | | |
| DR Pfam; PF00965; TIMP; 1. | | | |
| DR SMART; SM00206; NTR; 1. | | | |
| DR PROSITE; PS0189; NTR; 1. | | | |
| DR PROSITE; PS00288; TIMP; 1. | | | |
| KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation; | | | |
| Signal. | | | |
| FT SIGNAL | 1 | 23 | METALLOPROTEINASE INHIBITOR 1. |
| FT CHAIN | 24 | 206 | NTR. |
| FT DOMAIN | 24 | 147 | BY SIMILARITY. |
| FT DISULFID | 24 | 93 | BY SIMILARITY. |
| FT DISULFID | 26 | 122 | BY SIMILARITY. |
| FT DISULFID | 36 | 147 | BY SIMILARITY. |
| FT DISULFID | 150 | 196 | BY SIMILARITY. |
| FT DISULFID | 155 | 160 | BY SIMILARITY. |

FT DISULFID 168 188 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 206 AA; 22758 MW; 1839ABDE174EE9E CRC64;

Query Match 100.0%; Score 34; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 Db 24 CTCVP 28

RESULT 2

TIMI_BOVIN
 ID TIMI_BOVIN STANDARD; PRT; 207 AA.
 AC P20414; Q9TVB0;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-1).
 GN TIMP1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90365711; PubMed=2393392;
 RA Freudenstein J., Wagner S., Luck R.M., Einspanier R., Scheit K.H.;
 RT "mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue."
 RL Biochem. Biophys. Res. Commun. 171:250-256(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257757; PubMed=8199264;
 RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
 RT "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct cells enhances in vitro development of bovine embryo."
 RL Biol. Reprod. 50:835-844(1994).
 RN [3]
 RP SEQUENCE OF 25-191 FROM N.A.
 RC TISSUE-Skeletal muscle;
 RA Balcerzak D., Quereingesser L., Dixon W.T., Baracos V.E.;
 RT "Involvement of fibroblasts and muscle cells in the expression of an extracellular proteolytic cascade in bovine skeletal muscle."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP PRELIMINARY SEQUENCE OF 24-69.
 RX MEDLINE=90008914; PubMed=2551903;
 RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
 RT "Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells."
 RL J. Biol. Chem. 264:17445-17453(1989).
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of disulfide bonds.
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.

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CC EMBL; M60073; AAA30784.1; -;
 CC EMBL; S70841; AAB30892.1; -;
 DR EMBL; AF144763; AAD30303.1; -;
 DR PIR; A35685; A35685.
 DR HSSP; P01033; IUEA.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 KW Signal.
 FT SIGNAL 1 23 METALLOPROTEINASE INHIBITOR 1.
 FT CHAIN 24 207 NTR.
 FT DOMAIN 24 147 BY SIMILARITY.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 207 AA; 23031 MW; E672BEE2E865F3F7 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 Db 24 CTCVP 28

RESULT 3

TIMI_HORSE
 ID TIMI_HORSE STANDARD; PRT; 207 AA.
 AC O02722;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=99074117; PubMed=9858406;
 RA Richardson D.W., Dodge G.R.;
 RT "Molecular characteristics of equine stromelysin and the tissue inhibitor of metalloproteinase 1."
 RL Am. J. Vet. Res. 59:1557-1562(1998).
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of disulfide bonds (By similarity).
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.

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CC EMBL; U95039; AAB53735.1; -
DR HSP; P01033; 1UEA.
DR InterPro; IPR001820; TIMP.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS00189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
KW Signal.
FT CHAIN 1 23 BY SIMILARITY.
FT DOMAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
FT CHAIN 24 147 NTR.
FT DISULFID 24 93 BY SIMILARITY.
FT DISULFID 26 122 BY SIMILARITY.
FT DISULFID 36 147 BY SIMILARITY.
FT DISULFID 150 197 BY SIMILARITY.
FT DISULFID 155 160 BY SIMILARITY.
FT DISULFID 168 189 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 207 AA; 23046 MW; PD710DA98D168070 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
DB 24 CTCVP 28

RESULT 4
TIMP_HUMAN STANDARD; PRT; 207 AA.
ID TIMP_HUMAN STANDARD; PRT; 207 AA.
AC P01033; Q14252; Q9UCU1;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Metalloprotease inhibitor 1 precursor (TIMP-1) (Erythroid
DE potentiating activity) (EPA) (Tissue inhibitor of metalloproteinases)
DE (Fibroblast collagenase inhibitor) (Collagenase inhibitor).
GN TIMP OR TIMP OR CLGI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=86040463; PubMed=3903517;
RX Doeherty A.J.P., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,
RA Harris T.J.R., Murphy G., Reynolds J.J.;
RT "Sequence of human tissue inhibitor of metalloproteinases and its
RT identity to erythroid-potentiating activity.";
RL Nature 318:66-69 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85240567; PubMed=3839290;
RA Gasson J.C., Golde D.W., Kaufman S.E., Westbrook C.A., Hewick R.M.,
RA Kaufman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,
RA Orr E.C., Clark S.C.;
RT "Molecular characterization and expression of the gene encoding human
RT erythroid-potentiating activity.";
RL Nature 315:768-771 (1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205964; PubMed=3010309;
RA Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,
RA Welgus H.G., Stricklin G.P.;
RT "Primary structure and cDNA cloning of human fibroblast collagenase
RT inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411 (1986).

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RN [4]
RP SEQUENCE FROM N.A.
RA Kaczorek M., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,
RA Streeck R.E.;
RT "Molecular cloning and synthesis of biologically active human tissue
RT inhibitor of metalloproteinases in yeast.";
RL Biotechnology 5:595-598 (1987).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=91025550; PubMed=2171551;
RA Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,
RA Scheit K.H.;
RT "Characterization of three abundant mRNAs from human ovarian
RT granulosa cells.";
RL DNA Cell Biol. 9:479-485 (1990).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=94123576; PubMed=7507419;
RA Opbroek A., Kenney M.C., Brown D.;
RT "Characterization of a human corneal metalloproteinase inhibitor
RT (TIMP-1)."
RL Curr. Eye Res. 12:877-883 (1993).
RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [8]
RP SEQUENCE OF 42-207 FROM N.A.
RA Matsuda T., Kohno K., Kuwano M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 1-40 FROM N.A.
RA Harcastle A.J.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [10]
RP DISULFIDE BONDS, AND PARTIAL SEQUENCE.
RX MEDLINE=90303199; PubMed=2163605;
RA Williamson R.A., Martson F.A.O., Angal S., Koklitis P., Panico M.,
RA Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;
RT "Disulphide bond assignment in human tissue inhibitor of
RT metalloproteinases (TIMP)."
RL Biochem. J. 268:267-274 (1990).
RN [11]
RP SEQUENCE OF 24-38.
RC TISSUE=Synovial fluid;
RX MEDLINE=92111776; PubMed=1730286;
RA Othues A., Knaeuper V., Oberhoff R., Reinke H., Tschesche H.;
RT "Isolation and characterization of tissue inhibitors of
RT metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial
RT fluid."
RL FEBS Lett. 296:16-20 (1992).
RN [12]

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SEQUENCE OF 24-52.
 RX MEDLINE=91355647; PubMed=1653055;
 RA Van Ranst M., Norga K., Maure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., Van Damme J., Odenakker G.;
 RT "The cytokine-protease connection: Identification of a 96-kD THP-1
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239(1991).
 [13]
 RN MUTAGENESIS.
 RX MEDLINE=93041700; PubMed=1420137;
 RA O'Shea M., Willenbrock F., Williamson R.A., Cockett M.I.,
 RA Freedman R.B., Reynolds J.J., Docherty A.J.P., Murphy G.;
 RT "Site-directed mutations that alter the inhibitory activity of the
 RT tissue inhibitor of metalloproteinases-1: importance of the
 RT N-terminal region between cysteine 3 and cysteine 13.";
 RL Biochemistry 31:10146-10152(1992).
 [14]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH MMP-3.
 RX MEDLINE=97433330; PubMed=9288970;
 RA Gomis-Ruth F.X., Maskos K., Betz M., Beigner A., Huber R., Suzuki K.,
 RA Yoshida N., Nagase H., Brew K., Bourenkov G.P., Bartunik H., Bode W.;
 RT "Mechanism of inhibition of the human matrix metalloproteinase
 RT stromelysin-1 by TIMP-1.";
 RL Nature 389:77-81(1997).
 [15]
 RN STRUCTURE BY NMR OF 24-149.
 RX MEDLINE=20090931; PubMed=10623524;
 RA Wu B., Arumugam S., Gao G., Lee G.I., Semchenko V., Huang W.,
 RA Brew K., Van Doren S.R.;
 RT "NMR structure of tissue inhibitor of metalloproteinases-1 implicates
 RT localized induced fit in recognition of matrix metalloproteinases.";
 RL J. Mol. Biol. 295:257-268(2000).
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
 CC AND IRREVERSIBLY INACTIVATES THEM. ALSO MEDIATES ERYTHROPOIESIS IN
 CC VITRO; BUT, UNLIKE IL-3, IT IS SPECIES-SPECIFIC, STIMULATING THE
 CC GROWTH AND DIFFERENTIATION OF ONLY HUMAN AND MURINE ERYTHROID
 CC PROGENITORS. KNOWN TO ACT ON MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,
 CC MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 AND MMP-16. DOES NOT ACT ON
 CC MMP-14.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of
 CC disulfide bonds.
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC
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 CC EMBL; X03124; CAA26902.1; -
 CC EMBL; M12670; AAS2436.1; -
 CC EMBL; X02598; CAA26443.1; -
 CC EMBL; M59906; AAG3234.1; -
 CC EMBL; S68252; AAD14009.1; -
 CC EMBL; BC000866; AAB00866.1; -
 CC EMBL; D11139; BAA01913.1; -
 CC EMBL; I47361; AAY5558.1; -
 CC EMBL; A10416; CAA00898.1; -
 CC PIR; A93372; ZYHUFP.
 CC PDB; 1UEA; 25-NOV-98.
 CC PDB; 1D2B; 22-DEC-99.
 CC PDB; 1LQN; 05-JUN-02.
 CC GlycoSuiteDB; P01033; -
 CC Gnew; HGNC:11820; TIMP1.
 CC MIM; 305370; -
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0008191; F:metalloendopeptidase inhibitor activity; TAS.
 CC GO; GO:0008237; F:metalloproteinase activity; NAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;
 KW 3D-structure; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT DOMAIN 24 147 NTR.
 FT DISULFID 24 93
 FT DISULFID 26 122
 FT DISULFID 36 147
 FT DISULFID 150 197
 Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No 7.4; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTCVP 5
 Db 24 CTCVP 28
 RESULT 5
 TIM1_PAPCY STANDARD; PRT; 207 AA.
 ID TIM1_PAPCY
 AC P49061;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Papio cynocephalus (Yellow baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OC NCBI_TaxID=9556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=96011646; PubMed=7590279;
 RA Forough R., Nikkari S.F., Hasenstab D., Lea H., Clowes A.W.;
 RT "Cloning and characterization of a cDNA encoding the baboon tissue
 RT inhibitor of matrix metalloproteinase-1 (TIMP-1).";
 RL Gene 163:267-271(1995).
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of
 CC disulfide bonds.
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC
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 CC
 CC EMBL; L37295; AAA99943.1; -
 CC HSSP; P01033; 1D2B.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SM00206; NTR; 1.
 DR PROSITE; PS50189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloprotease inhibitor; Erythrocyte maturation;

KW Signal. 1 23 BY SIMILARITY.
 FT SIGNAL 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT CHAIN 24 147 NTR.
 FT DOMAIN 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 189 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 207 AA; 23213 MW; 5AB4FDBEAB2ECDC CRC64;
 Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 24 CTCVP 28
 RESULT 6
 ID TIM1_PIG STANDARD; PRT; 207 AA.
 AC P35624; Q9TTB9; 29, Created
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=92201478; PubMed=1312961;
 RA Tanaka T., Andoh N., Takeya T., Sato E.;
 RT "Differential screening of ovarian cDNA libraries detected the
 RT expression of the porcine collagenase inhibitor gene in functional
 RT corpora lutea.";
 RL Mol. Cell. Endocrinol. 83:65-71(1992).
 RN [2]
 RP SEQUENCE OF 34-195 FROM N.A.
 RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
 RT "Gene expression level of mmp3 and Timpi in intervertebral disc.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 37-144 FROM N.A.
 RC TISSUE=Skin;
 RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
 RT "Cloning and sequencing of porcine TIMPs.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: The activity of TIMP1 is dependent on the presence of
 CC disulfide bonds.
 CC -!- SIMILARITY: Belongs to the TIMP family.
 CC -!- SIMILARITY: Contains 1 NTR domain.
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 CC EMBL; S96211; AAB21865.1; -.

DR EMBL; AF201726; AAF24348.1; -.
 DR EMBL; AF156029; AAF17354.1; -.
 DR PIR; I47061; I47061.
 DR HSSP; P01033; IUEA.
 DR InterPro; IPR001820; TIMP.
 DR InterPro; IPR008993; TIMP_like.
 DR Pfam; PF00965; TIMP; 1.
 DR SMART; SMO0206; NTR; 1.
 DR PROSITE; PS00189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KW Glycoprotein; Metalloproteinase inhibitor; Erythrocyte maturation;
 KW Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 FT DOMAIN 24 147 NTR.
 FT DISULFID 24 93 BY SIMILARITY.
 FT DISULFID 26 122 BY SIMILARITY.
 FT DISULFID 36 147 BY SIMILARITY.
 FT DISULFID 150 197 BY SIMILARITY.
 FT DISULFID 155 160 BY SIMILARITY.
 FT DISULFID 168 189 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 34 34 A -> P (IN REF. 2).
 FT CONFLICT 37 37 S -> N (IN REF. 3).
 FT CONFLICT 41 41 V -> F (IN REF. 2).
 FT CONFLICT 59 59 K -> Q (IN REF. 1).
 FT CONFLICT 86 86 T -> A (IN REF. 3).
 FT CONFLICT 141 142 EI -> KT (IN REF. 3).
 SQ SEQUENCE 207 AA; 23098 MW; B04895846EB56BD0 CRC64;
 Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 24 CTCVP 28
 RESULT 7
 ID TIM1_SHEEP STANDARD; PRT; 207 AA.
 AC P50122; 34, Created
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN TIMP1.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Corpus luteum;
 RX MEDLINE=94102210; PubMed=8275949;
 RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;
 RT "Molecular cloning of an ovine ovarian tissue inhibitor of
 RT metalloproteinases: ontogeny of messenger ribonucleic acid expression
 RT and in situ localization within preovulatory follicles and luteal
 RT tissue.";
 RL Endocrinology 134:344-352(1994).
 CC -!- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: The activity of TIMP1 is dependent on the presence of
 CC disulfide bonds.
 CC -!- SIMILARITY: Belongs to the TIMP family.
 CC -!- SIMILARITY: Contains 1 NTR domain.
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EMBL; S67450; AAB29472.1; -
 PIR; I46964; I46964.
 HSSP; P01033; IUEA.
 InterPro; IPR001820; TIMP.
 InterPro; IPR008993; TIMP_like.
 Pfam; PF00965; TIMP; 1.
 SMART; SM00206; NTR; 1.
 PROSITE; PS50189; NTR; 1.
 PROSITE; PS00288; TIMP; 1.
 GlycoProtein; Metalloprotease inhibitor; Erythrocyte maturation; Signal.
 SIGNAL 1 23 BY SIMILARITY.
 CHAIN 24 207 METALLOPROTEINASE INHIBITOR 1.
 DOMAIN 24 147 NTR.
 DISULFID 24 93 BY SIMILARITY.
 DISULFID 26 122 BY SIMILARITY.
 DISULFID 36 147 BY SIMILARITY.
 DISULFID 150 197 BY SIMILARITY.
 DISULFID 155 160 BY SIMILARITY.
 DISULFID 168 189 BY SIMILARITY.
 CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 207 AA; 23057 MW; 103BCA2012F80E46 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 Db 24 CTCVP 28

RESULT 8
 ID TIM3 CHICK
 AC P26652; STANDARD; PRT; 212 AA.
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Metalloprotease inhibitor 3 precursor (TIMP-3) (Tissue inhibitor of metalloproteases-3) (21 kDa protein of extracellular matrix).
 DE TIMP3 OR IMP-3.
 GN Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic fibroblast;
 RX MEDLINE=92381050; PubMed=1512267;
 RA Pavloff N., Staskus P.W., Kishanani N.S., Hawkes S.P.;
 RT "A new inhibitor of metalloproteinases from chicken: ChIMP-3. A third member of the TIMP family.";
 RL J. Biol. Chem. 267:17321-17326(1992).
 RN [2]
 RP SEQUENCE OF 25-53.
 RC TISSUE=Fibroblast;
 RX MEDLINE=91093162; PubMed=1845973;
 RA Staskus P.W., Nasirz F.R., Fallanck L.J., Hawkes S.P.;
 RT "The 21-kDa protein is a transformation-sensitive metalloproteinase inhibitor of chicken fibroblasts.";
 RL J. Biol. Chem. 266:449-454(1991).
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them. May form part of a tissue-

specific acute response to remodeling stimuli.
 -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 -1- SIMILARITY: Belongs to the TIMP family.
 -1- SIMILARITY: Contains 1 NTR domain.

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EMBL; M94531; AAA48813.1; -
 PIR; A43429; A43429.
 HSSP; P16035; IBR9.
 InterPro; IPR001820; TIMP.
 InterPro; IPR008993; TIMP_like.
 Pfam; PF00965; TIMP; 1.
 SMART; SM00206; NTR; 1.
 PROSITE; PS50189; NTR; 1.
 PROSITE; PS00288; TIMP; 1.
 Metalloprotease inhibitor; Signal.
 SIGNAL 1 24
 CHAIN 25 212 METALLOPROTEINASE INHIBITOR 3.
 DOMAIN 25 144 NTR.
 DISULFID 25 92 BY SIMILARITY.
 DISULFID 27 119 BY SIMILARITY.
 DISULFID 37 144 BY SIMILARITY.
 DISULFID 146 193 BY SIMILARITY.
 DISULFID 151 156 BY SIMILARITY.
 DISULFID 164 185 BY SIMILARITY.
 SEQUENCE 212 AA; 24504 MW; 17F159ADE108D618 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
 Db 25 CTCVP 29

RESULT 9
 ID PGCV MACNE
 AC Q28858; Q28859; Q28860; STANDARD; PRT; 862 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Versican core protein (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (Fragments).
 DE CSFG2.
 GN Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Arctic smooth muscle;
 RX MEDLINE=95005762; PubMed=7921538;
 RA Yao L.Y., Moody C., Schoenher E., Wight T.N., Sandell L.J.;
 RT "Identification of the proteoglycan versican in aorta and smooth muscle cells by DNA sequence analysis, in situ hybridization and immunohistochemistry.";
 RL Matrix Biol. 14:213-225(1994).
 CC -1- FUNCTION: May play a role in intercellular signaling and in connecting cells with the extracellular matrix. May take part in the regulation of cell motility, growth and differentiation. Binds hyaluronan.
 CC -1- SUBUNIT: Interacts with FBLN1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By


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Db          542 CTCVP 546

RESULT 11
CRB_DROME
ID CRB_DROME STANDARD; PRT; 2139 AA.
AC P10040;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Crumbs protein precursor (95F).
GN CRB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Oregon-R; TISSUE=Embryo;
RC MEDLINE=90263104; PubMed=2344615;
RA Tepass U., Theres C., Knust E.;
RT "Crumbs encodes an EGF-like protein expressed on apical membranes of
RT Drosophila epithelial cells and required for organization of
RT epithelia.";
RL Cell 61:787-799(1990).
RN [2]
SEQUENCE OF 1663-1955 FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=87218537; PubMed=3107985;
RA Knust E., Dietrich U., Tepass U., Bremer K.A., Weigelt D.,
RA Vaessin H., Campos-Ortega J.A.;
RT "EGF homologous sequences encoded in the genome of Drosophila
RT melanogaster, and their relation to neurogenic genes.";
RL EMBO J. 6:761-766(1987).
CC -!- FUNCTION: May play a role in the development of epithelia,
CC possibly for the establishment and/or maintenance of cell
CC polarity. It may act as a signal.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: PHOSPHORYLATED IN THE CYTOPLASMIC DOMAIN (POTENTIAL).
CC -!- SIMILARITY: Contains 29 EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M33753; AAA28428.1; ALT_SEQ.
DR EMBL; X05144; CAA28793.1; -.
DR PIR; A35672; A35672.
DR PIR; B26637; B26637.
DR HSP; P00740; IEDM.
DR FlyBase; FBgn000368; crb.
DR GO; GO:0016324; C:apical plasma membrane; NAS.
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. . ; IMP.
DR GO; GO:0016332; P:establishment and/or maintenance of polarit. . ; IMP.
DR GO; GO:0016334; P:establishment and/or maintenance of polarit. . ; IMP.
DR GO; GO:0045494; P:photoreceptor maintenance; NAS.
DR GO; GO:0042052; P:rhabdomere development; NAS.
DR GO; GO:0045186; P:zonula adherens assembly; IMP.
DR GO; GO:0045218; P:zonula adherens maintenance; IMP.
DR InterPro; IPR000152; Aex_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR Pfam; PF00008; EGF; 26.
DR Pfam; PF00054; laminin_G; 3.
DR PRINTS; PRO0010; EGFELOOD.
DR PRINTS; PRO0011; EGFLAMININ.
DR SMART; SM00179; EGF_CA; 11.
DR SMART; SM00282; LamG; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 15.
DR PROSITE; PS00022; EGF_1; 26.
DR PROSITE; PS01186; EGF_2; 17.
DR PROSITE; PS00026; EGF_3; 27.
DR PROSITE; PS01187; EGF_CA; 12.
DR PROSITE; PS00025; LAM_G_DOMAIN; 3.
KW Differentiation; Repeat; EGF-like domain; Transmembrane;
KW Glycoprotein; Signal; Phosphorylation.
FT SIGNAL 1 90
FT CHAIN 91 2139 CRUMBS PROTEIN.
FT DOMAIN 91 2084 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 2085 2111 POTENTIAL.
FT DOMAIN 2112 2139 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 267 303 EGF-LIKE 1.
FT DOMAIN 306 343 EGF-LIKE 2.
FT DOMAIN 348 386 EGF-LIKE 3.
FT DOMAIN 388 425 EGF-LIKE 4.
FT DOMAIN 427 463 EGF-LIKE 5.
FT DOMAIN 464 500 EGF-LIKE 6.
FT DOMAIN 501 532 EGF-LIKE 7.
FT DOMAIN 545 581 EGF-LIKE 8.
FT DOMAIN 582 611 EGF-LIKE 9.
FT DOMAIN 609 646 EGF-LIKE 10.
FT DOMAIN 648 685 EGF-LIKE 11.
FT DOMAIN 687 723 EGF-LIKE 12.
FT DOMAIN 725 761 EGF-LIKE 13.
FT DOMAIN 763 800 EGF-LIKE 14.
FT DOMAIN 802 838 EGF-LIKE 15.
FT DOMAIN 840 902 EGF-LIKE 16.
FT DOMAIN 904 940 EGF-LIKE 17.
FT DOMAIN 942 978 EGF-LIKE 18.
FT DOMAIN 980 1021 EGF-LIKE 19.
FT DOMAIN 1023 1205 LAMININ G-LIKE 1.
FT DOMAIN 1207 1243 EGF-LIKE 20.
FT DOMAIN 1250 1280 LAMININ G-LIKE 2.
FT DOMAIN 1481 1517 EGF-LIKE 21.
FT DOMAIN 1558 1758 LAMININ G-LIKE 3.
FT DOMAIN 1759 1795 EGF-LIKE 22.
FT DOMAIN 1797 1833 EGF-LIKE 23.
FT DOMAIN 1835 1871 EGF-LIKE 24.
FT DOMAIN 1874 1915 EGF-LIKE 25.
FT DOMAIN 1915 1951 EGF-LIKE 26.
FT DOMAIN 1953 1989 EGF-LIKE 27.
FT DOMAIN 1991 2029 EGF-LIKE 28.
FT DOMAIN 2030 2070 EGF-LIKE 29.
FT DISULFID 271 282 BY SIMILARITY.
FT DISULFID 276 291 BY SIMILARITY.
FT DISULFID 293 302 BY SIMILARITY.
FT DISULFID 310 321 BY SIMILARITY.
FT DISULFID 315 331 BY SIMILARITY.
FT DISULFID 333 342 BY SIMILARITY.
FT DISULFID 352 363 BY SIMILARITY.
FT DISULFID 357 374 BY SIMILARITY.
FT DISULFID 376 385 BY SIMILARITY.
FT DISULFID 392 403 BY SIMILARITY.
FT DISULFID 397 412 BY SIMILARITY.
FT DISULFID 414 424 BY SIMILARITY.
FT DISULFID 431 442 BY SIMILARITY.
FT DISULFID 436 451 BY SIMILARITY.
FT DISULFID 453 462 BY SIMILARITY.
FT DISULFID 468 479 BY SIMILARITY.
FT DISULFID 473 488 BY SIMILARITY.
FT DISULFID 490 499 BY SIMILARITY.
FT DISULFID 505 515 BY SIMILARITY.
FT DISULFID 509 520 BY SIMILARITY.
FT DISULFID 522 531 BY SIMILARITY.

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FT DISULFID 549 BY SIMILARITY. 562
 FT DISULFID 556 BY SIMILARITY. 569
 FT DISULFID 571 BY SIMILARITY. 580
 FT DISULFID 586 BY SIMILARITY. 597
 FT DISULFID 591 BY SIMILARITY. 602
 FT DISULFID 604 BY SIMILARITY. 610
 FT DISULFID 624 BY SIMILARITY. 624
 FT DISULFID 613 BY SIMILARITY. 634
 FT DISULFID 618 BY SIMILARITY. 645
 FT DISULFID 636 BY SIMILARITY. 664
 FT DISULFID 652 BY SIMILARITY. 673
 FT DISULFID 659 BY SIMILARITY. 673
 FT DISULFID 675 BY SIMILARITY. 684
 FT DISULFID 691 BY SIMILARITY. 702
 FT DISULFID 696 BY SIMILARITY. 711
 FT DISULFID 713 BY SIMILARITY. 722
 FT DISULFID 729 BY SIMILARITY. 740
 FT DISULFID 734 BY SIMILARITY. 749
 FT DISULFID 751 BY SIMILARITY. 760
 FT DISULFID 767 BY SIMILARITY. 778
 FT DISULFID 772 BY SIMILARITY. 787
 FT DISULFID 789 BY SIMILARITY. 799
 FT DISULFID 806 BY SIMILARITY. 817
 FT DISULFID 811 BY SIMILARITY. 826
 FT DISULFID 828 BY SIMILARITY. 837
 FT DISULFID 844 BY SIMILARITY. 855
 FT DISULFID 849 BY SIMILARITY. 890
 FT DISULFID 892 BY SIMILARITY. 901
 FT DISULFID 908 BY SIMILARITY. 913
 FT DISULFID 930 BY SIMILARITY. 939
 FT DISULFID 946 BY SIMILARITY. 957
 FT DISULFID 952 BY SIMILARITY. 966
 FT DISULFID 968 BY SIMILARITY. 977
 FT DISULFID 984 BY SIMILARITY. 995
 FT DISULFID 989 BY SIMILARITY. 1009
 FT DISULFID 1011 BY SIMILARITY. 1020
 FT DISULFID 1211 BY SIMILARITY. 1222
 FT DISULFID 1216 BY SIMILARITY. 1231
 FT DISULFID 1233 BY SIMILARITY. 1242
 FT DISULFID 1485 BY SIMILARITY. 1496
 FT DISULFID 1490 BY SIMILARITY. 1505
 FT DISULFID 1507 BY SIMILARITY. 1516
 FT DISULFID 1763 BY SIMILARITY. 1774
 FT DISULFID 1768 BY SIMILARITY. 1783
 FT DISULFID 1785 BY SIMILARITY. 1794
 FT DISULFID 1801 BY SIMILARITY. 1812
 FT DISULFID 1806 BY SIMILARITY. 1821
 FT DISULFID 1823 BY SIMILARITY. 1832
 FT DISULFID 1839 BY SIMILARITY. 1850
 FT DISULFID 1844 BY SIMILARITY. 1859
 FT DISULFID 1861 BY SIMILARITY. 1870
 FT DISULFID 1878 BY SIMILARITY. 1889
 FT DISULFID 1883 BY SIMILARITY. 1903
 FT DISULFID 1905 BY SIMILARITY. 1914
 FT DISULFID 1919 BY SIMILARITY. 1930
 FT DISULFID 1924 BY SIMILARITY. 1939
 FT DISULFID 1941 BY SIMILARITY. 1950
 FT DISULFID 1957 BY SIMILARITY. 1968
 FT DISULFID 1962 BY SIMILARITY. 1977

Query Match 100.0%; Score 34; DB 1; Length 2139;
 Best Local Similarity 100.0%; Pred. NO. 66;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCVP 5
 |||||
 Db 1903 CTCVP 1907

RESULT 12
 PGCV BOVIN
 ID FGCV BGWIN STANDARD; PRT: 3381 AA.
 AC P81282; 077609; 077610; 077611; 077612;

DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Versican core protein precursor (large fibroblast proteoglycan)
 DE Chondroitin sulfate proteoglycan core protein 2 (PG-M) (Glia)
 DE hyaluronate-binding protein) (GHAP).
 GN CPBG2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS VO; V1; V2 AND V3).
 RC TISSUE=Forebrain;
 RX MEDLINE=98288320; PubMed=9624174;
 RA Schmalfeidt M., Dours-Zimmermann M.T., Winterhalter K.H.,
 RA Zimmermann D.R.;
 RT "Versican V2 is a major extracellular matrix component of the mature
 RT bovine brain."
 RL J. Biol. Chem. 273:15758-15764(1998).
 RN [2]
 RP SEQUENCE OF 21-53; 78-96; 226-250; 262-277; 295-306; 314-324; 329-331
 RP AND 342-348.
 RC TISSUE=Spinal cord;
 RX MEDLINE=92062692; PubMed=1720020;
 RA Perides G., Biviano F., Signami A.;
 RT "Interaction of a brain extracellular matrix protein with hyaluronic
 RT acid."
 RL Biochim. Biophys. Acta 1075:248-258(1991).
 CC -!- FUNCTION: May play a role in intercellular signaling and in
 CC connecting cells with the extracellular matrix. May take part in
 CC the regulation of cell motility, growth and differentiation. Binds
 CC hyaluronic acid.
 CC -!- SUBUNIT: Interacts with FBLN1 (by similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=V0;
 CC IsoId=P81282-1; Sequence=Displayed;
 CC Name=V1;
 CC IsoId=P81282-2; Sequence=VSP_003078, VSP_003079;
 CC Name=V2;
 CC IsoId=P81282-3; Sequence=VSP_003080;
 CC Name=V3;
 CC IsoId=P81282-4; Sequence=VSP_003078, VSP_003081;
 CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 are expressed
 CC in the central nervous system, and in a number of mesenchymal and
 CC epithelial tissues; the major isoform V2 is restricted to the
 CC central nervous system.
 CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development
 CC (by similarity).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 link domains.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
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 CC -----
 CC EMBL; AF060456; AAC24358.1; -;
 CC EMBL; AF060457; AAC24359.1; -;
 CC EMBL; AF060458; AAC24360.1; -;
 CC EMBL; AF060459; AAC24361.1; -;
 CC FIC; T14274; T14274.

DR PIR; T42389; T42389.
 DR HSP; P01132; IEPG.
 DR InterPro; IPR000152; Asx hydroxylase.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR000538; Link.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00059; lectin_c; 1.
 DR Pfam; PF00084; sushi; 1.
 DR Pfam; PF00193; Xlink; 2.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 2.
 DR SMART; SM00032; CCF; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF CA; 1.
 DR SMART; SM00409; IG_1.
 DR SMART; SM00445; LINK; 2.
 DR PROSITE; PS00010; ASX HYDROXYL; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS00641; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 2.
 DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 DR PROSITE; PS01241; LINK; 2.
 DR GlycoProtein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
 KW Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
 KW Hyaluronic acid; Alternative splicing.
 FT SIGNAL 1 20
 FT CHAIN 21 3381
 FT DOMAIN 21 147
 FT DOMAIN 168 245
 FT DOMAIN 266 347
 FT DOMAIN 349 1336
 FT DOMAIN 1337 3074
 FT DOMAIN 3074 3110
 FT DOMAIN 3112 3148
 FT DOMAIN 3161 3275
 FT DOMAIN 3280 3338
 FT DISULFID 44 131
 FT DISULFID 173 244
 FT DISULFID 197 218
 FT DISULFID 271 346
 FT DISULFID 295 316
 FT DISULFID 3078 3089
 FT DISULFID 3083 3098
 FT DISULFID 3100 3109
 FT DISULFID 3116 3127
 FT DISULFID 3121 3136
 FT DISULFID 3128 3147
 FT DISULFID 3154 3165
 FT DISULFID 3182 3274
 FT DISULFID 3250 3266
 FT DISULFID 3281 3324
 FT DISULFID 3310 3337
 FT CARBOHYD 57 57
 FT CARBOHYD 331 331
 FT CARBOHYD 352 352
 FT CARBOHYD 817 817
 FT CARBOHYD 965 965
 FT CARBOHYD 1017 1017
 FT CARBOHYD 1333 1333
 FT CARBOHYD 1393 1393
 FT CARBOHYD 1437 1437
 FT CARBOHYD 1463 1463

FT CARBOHYD 1653 1653
 FT CARBOHYD 1974 1974
 FT CARBOHYD 2045 2045
 FT CARBOHYD 2074 2074
 FT CARBOHYD 2103 2103
 FT CARBOHYD 2263 2263
 FT CARBOHYD 2290 2290
 FT CARBOHYD 2356 2356
 FT CARBOHYD 2623 2623
 FT CARBOHYD 2641 2641
 FT CARBOHYD 2919 2919
 FT CARBOHYD 3052 3052
 FT CARBOHYD 3354 3354
 FT CARBOHYD 3364 3364
 FT VARSPPLIC 349 349
 FT VARSPPLIC 350 1336
 FT VARSPPLIC 1337 3074
 FT VARSPPLIC 350 3074
 FT CONFLICT 25 25
 FT CONFLICT 51 51
 FT CONFLICT 89 89
 FT CONFLICT 96 96
 FT CONFLICT 346 346
 FT SEQUENCE 3381 AA; 369984 MW; F09716FA778D459 CRC64;
 SQ SEQUENCE 100.0%; Score 34; DB 1; Length 3381;
 Query Match 100.0%; Pred. No. 1e+02;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Indels 0; Gaps 0;
 QY 1 CTCVP 5
 Db 3098 CTCVP 3102
 RESULT 13
 PGCV HUMAN STANDARD; PRT; 3396 AA.
 ID PGCV HUMAN Q13010; Q13189; Q15123; Q9UNW5;
 AC P13611; P20754; Q13010; Q13189; Q15123; Q9UNW5;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Versican core protein precursor (large fibroblast proteoglycan)
 DE (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glia)
 DE hyaluronate-binding protein) (GHAP).
 GN CSFG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM V0).
 RX MEDLINE=95105186; PubMed=7528742;
 RA Naso M.F., Zimmermann D.R., Iozzo R.V.;
 RT "Characterization of the complete genomic structure of the human
 RT versican gene and functional analysis of its promoter.";
 RL J. Biol. Chem. 269:32999-33008(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM V1).
 RC TISSUE=Placenta;
 RX MEDLINE=90059882; PubMed=2583089;
 RA Zimmermann D.R., Ruoslahti E.;
 RT "Multiple domains of the large fibroblast proteoglycan, versican.";
 RL EMBO J. 8:2975-2981(1989).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM V2).
 RC TISSUE=Glia; tumor;
 RX MEDLINE=95105187; PubMed=7806529;
 RA Dours-Zimmermann M.T., Zimmermann D.R.;
 RT "A novel glycosaminoglycan attachment domain identified in two

RT alternative splice variants of human versican.";
RL J. Biol. Chem. 269:32992-32998(1994).
RN [4]
RP SEQUENCE OF 2711-3396 FROM N.A.
RC TISSUE=Lung fibroblast;
RX MEDLINE=88007514; PubMed=2820964;
RA Kruusius T., Gehlsen K.R., Ruoslahti E.;
RT "A fibroblast chondroitin sulfate proteoglycan core protein contains
RL lectin-like and growth factor-like sequences.";
RJ J. Biol. Chem. 262:13120-13125(1987).
RN [5]
RP SEQUENCE OF 251-347 FROM N.A.
RX MEDLINE=93122792; PubMed=1478664;
RA Iozzo R.V., Naso M.F., Cannizzaro L.A., Wasmuth J.J.,
RA McPherson J.D.;
RT "Mapping of the versican proteoglycan gene (CSPG2) to the long arm of
RL human chromosome 5 (5q12-5q14).";
RJ Genomics 14:845-851(1992).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM V3).
RC TISSUE=Brain;
RX MEDLINE=95181355; PubMed=7876137;
RA Zako M., Shinomura T., Ujita M., Ito K., Kimata K.;
RT "Expression of PG-M(V3), an alternatively spliced form of PG-M
RL without a chondroitin sulfate attachment in region in mouse and human
RJ tissues.";
RJ J. Biol. Chem. 270:3914-3918(1995).
RN [7]
RP SEQUENCE OF 3333-3396 FROM N.A. (ISOFORM VINT).
RC TISSUE=Aortic smooth muscle;
RX MEDLINE=99327053; PubMed=10397680;
RA Lemire J.W., Braun K.R., Maurel P., Kaplan E.D., Schwartz S.M.,
RA Wright T.N.;
RT "Versican/PG-M isoforms in vascular smooth muscle cells.";
RL Arterioscler. Thromb. Vasc. Biol. 19:1630-1639(1999).
RN [8]
RP PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=89174663; PubMed=2466833;
RA Perides G., Lane W.S., Andrews D., Dahl D., Bignami A.;
RT "Isolation and partial characterization of a glial
RL hyaluronate-binding protein.";
RJ J. Biol. Chem. 264:5981-5987(1989).
RN [9]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=96213482; PubMed=8627343;
RA Paulus W., Baur I., Dours-Zimmermann M.T., Zimmermann D.R.;
RT "Differential expression of versican isoforms in brain tumors.";
RJ J. Neuropathol. Exp. Neurol. 55:528-533(1996).
CC -!- FUNCTION: May play a role in intercellular signaling and in
CC connecting cells with the extracellular matrix. May take part in
CC the regulation of cell motility, growth and differentiation. Binds
CC hyaluronic acid.
CC -!- SUBUNIT: Interacts with PBLN1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=V0;
CC IsoId=P13611-1; Sequence=Displayed;
CC Name=V1;
CC IsoId=P13611-2; Sequence=VSP_003082, VSP_003083;
CC Name=V2;
CC IsoId=P13611-3; Sequence=VSP_003084;
CC Name=V3;
CC IsoId=P13611-4; Sequence=VSP_003082, VSP_003085;
CC Name=Vint;
CC IsoId=P13611-5; Sequence=VSP_003086;
CC -!- TISSUE SPECIFICITY: Cerebral white matter. V0 and V1 is expressed
CC in normal brain, gliomas, medulloblastomas, schwannomas,
CC neurofibromas, and meningiomas; V2 is restricted to normal brain
CC and gliomas; V3 is found in all these tissues except
CC medulloblastomas.

CC -!- DEVELOPMENTAL STAGE: Disappears after the cartilage development.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 link domains.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 Sushi (SCR) domain.
CC -!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
CC
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CC
CC EMBL; U16306; AAA65018.1; -
CC EMBL; X15998; CAA34128.1; -
CC EMBL; S52488; AAB24878.1; -
CC EMBL; U26555; AAA67565.1; -
CC EMBL; D32039; BAA06801.1; -
CC EMBL; J02814; AAA36437.1; -
CC EMBL; AF084545; AAD48545.1; -
CC PIR; S06014; A60979.
CC HSSP; P01132; 1EGF.
CC Genew; HGNC:2464; CSPG2.
CC MIM; 118661; -
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005540; F:hyaluronic acid binding; TAS.
CC GO; GO:0008037; P:cell recognition; TAS.
CC GO; GO:0007275; P:development; TAS.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR007110; IG_Like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR001304; Lectin_C.
CC InterPro; IPR000538; Link_C.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00084; lectin_C; 1.
CC Pfam; PF00084; sushi; 1.
CC Pfam; PF00193; Xlink; 2.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 2.
CC SMART; SM00032; CCP; 1.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00409; IG; 1.
CC SMART; SM00445; LINK; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00835; IG_Like; 1.
CC PROSITE; PS01241; LINK; 2.
CC Glycoprotein; Proteoglycan; Lectin; Extracellular matrix; Sushi;
CC Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain;
CC Hyaluronic acid; Alternative splicing.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 3396 VERSICAN CORE PROTEIN.
CC DOMAIN 21 146 IG-LIKE V-TYPE.
CC DOMAIN 167 244 LINK 1.
CC DOMAIN 265 346 LINK 2.
CC DOMAIN 348 1335 GAG-ALPHA
CC (GLUCOSAMINOGLYCAN ATTACHMENT DOMAIN).
CC DOMAIN 1336 3089 GAG-BETA.
CC DOMAIN 3089 3125 EGF-LIKE 1.
CC DOMAIN 3127 3163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

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FT DOMAIN 3176 3290 C-TYPE LECTIN.
FT DOMAIN 3295 3353 SUSHI.
FT DISULFID 44 130 BY SIMILARITY.
FT DISULFID 172 243 BY SIMILARITY.
FT DISULFID 196 217 BY SIMILARITY.
FT DISULFID 270 345 BY SIMILARITY.
FT DISULFID 294 315 BY SIMILARITY.
FT DISULFID 3093 3104 BY SIMILARITY.
FT DISULFID 3098 3113 BY SIMILARITY.
FT DISULFID 3115 3124 BY SIMILARITY.
FT DISULFID 3131 3142 BY SIMILARITY.
FT DISULFID 3136 3151 BY SIMILARITY.
FT DISULFID 3153 3162 BY SIMILARITY.
FT DISULFID 3169 3180 BY SIMILARITY.
FT DISULFID 3197 3289 BY SIMILARITY.
FT DISULFID 3265 3281 BY SIMILARITY.
FT DISULFID 3296 3339 BY SIMILARITY.
FT DISULFID 3325 3352 BY SIMILARITY.
FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 100.0%; Score 34; DB 1; Length 3396;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 3113 CTCVP 3117

RESULT 14
VMSA HPBV0
ID VMSA HPBV0 STANDARD; PRT; 226 AA.
AC P31873;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88297159; PubMed=2841200;
RA Rivkina M.B., Lunin V.G., Mahov A.M., Tikchonenko T.I., Kukain R.A.;
RT "Nucleotide sequence of integrated hepatitis B virus DNA and human
RT flanking regions in the genome of the PLC/PRP/5 cell line.";
RL Gene 64:285-296(1988).

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CC -----
DR EMBL; M21030; AAA45516.1; -
DR PIR; J04820; CAA28506.1; -
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25476 MW; BFC4329CF1720600 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 226;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 147 CTCIP 151

Search completed: April 8, 2004, 11:11:08
Job time : 4.16667 secs
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Qy 1 CTCVP 5
Db 147 CTCIP 151

RESULT 15
VMSA HPBV0
ID VMSA HPBV0 STANDARD; PRT; 226 AA.
AC P31868;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Major surface antigen.
GN S.
OS Hepatitis B virus (subtype ad).
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=31511;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89143494; PubMed=2465492;
RA Okamoto H., Omi S., Wang Y., Itoh Y., Tauda F., Tanaka T., Akahane Y.,
RA Miyakawa Y., Mayumi M.;
RT "The loss of subtypic determinants in alleles, d/y or w/r, on
RT hepatitis B surface antigen.";
RL Mol. Immunol. 26:197-205(1989).

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CC -----
DR EMBL; M27765; AAA45518.1; -
DR PIR; PLO053; SAVLAD.
DR InterPro; IPR000349; Hepvir_surfag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
FT CARBOHYD 3 3 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 226 AA; 25348 MW; AFC12BCF3B08DC83 CRC64;

Query Match 97.1%; Score 33; DB 1; Length 226;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCVP 5
Db 147 CTCIP 151

Search completed: April 8, 2004, 11:11:08
Job time : 4.16667 secs
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